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PATENT
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IN THE U.S. PATENT AND TRADEMARK OFFICE

APPLICANT: Rosenthal, Andre et al. CONF: 7286

SERIAL NO.: 09/647,377 GROUP: 1632

FILED: September 27, 2000 EXAMINER: PRIEBE, S.

FOR: NUCLEIC ACID MOLECULES ENCODING PROTEINS WHICH INFLUENCE BONE DEVELOPMENT

DECLARATION SUBMITTED UNDER 37 C.F.R. § 1.132

Honorable Commissioner
Of Patents and Trademarks
Washington, D.C. 20231

February 26, 2003

Sir:

I, Andreas Rump of the metaGen Pharmaceuticals GmbH, Germany, do hereby declare the following:

I have attached a copy of my curriculum vitae to this Declaration.

I am Research Scientist, of the Oncology Department and have conducted the experiments described below.

I am an co-inventor of the above referenced patent application and am familiar with the development, usages and properties of LOBO ("long-bone") proteins described therein.

I have read and understand the subject matter of the Office Action of September 3, 2002.

Appl. No. 09/647,377

The following comments are offered in support of the patentability of the instant invention.

I have performed two types of searches to demonstrate the similarity between the murine LOBO protein and the human homolog LOBO protein described in the instant invention. In the first search, I used LALIGN to compare both the protein and the DNA sequences of the murine and human LOBO sequences. This search was done using the complete sequence of the murine LOBO protein/DNA disclosed in the application and the partial sequence of the human as known at the time of filing as well as the complete sequence as determined after the filing date of the instant application. LALIGN compares two protein or DNA sequences for local similarity and shows the local sequence alignments. LALIGN uses code developed by X. Huang and W. Miller (Adv. Appl. Math. (1991) 12:337-357) for the "sim" program. LALIGN will report a specified number of alignments (the default is 10) between the two sequences and their scores. The results of these comparisons are attached hereto as Appendices I (comparison of the complete mouse sequences v. partial human sequences known at the time of filing) and II (comparison of the complete mouse sequences v. complete human sequences as determined after the application was filed).

The results in Appendix I indicate that the sequence identity between the LOBO Coding Sequences of the Mouse (complete) v. Man (partial) was 85.2%. The sequence identity between the Mouse (complete) v. Man (partial) in the LOBO Protein-Alignment was 88.1% and the protein sequence similarity was 94.8%. The results in Appendix II indicate that the sequence identity for the LOBO Coding Sequences of the Mouse (complete) and Man (complete) was 85.9%. The sequence identity between the Mouse (complete) and Man (complete) in the LOBO Protein-Alignment was 88.3% and the protein sequence similarity was 96.2%. The results in Appendix II which compares the Mouse (complete) to Man (complete) further demonstrates the high degree of conservation between the murine and human DNA and protein sequences.

Appl. No. 09/647,377

I also performed a BLAST search (See, Altschul, S. et al. (1997) "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402) to locate similar sequences using as query the complete mouse LOBO protein sequence shown as SEQ ID No: 9 in the present application (see Annex 1; 870 amino acid residues). The blast search was done via the NCBI website (<http://www.ncbi.nlm.nih.gov/BLAST/>) against the complete translated GenBank database on January 29, 2003 (blastP). The complete results are summarized in Table 2, where the Subject ID, accession number, brief description of the subject, a bit score and e-value are listed. This list is followed by an alignment of the query and subject sequences. Each alignment indicates the percent identity and percent similarity between the two aligned sequences. Table 1 lists the ten sequences having the most significant identities.

The blastP search, Protein query-Translated db [blastP] was done using the program BLASTP 2.2.5 (version from Nov-16-2002) with the following default parameters:

- a. Databases searched: non-redundant = nr (All non-redundant GenBank CDS translations + PDB =[Sequences derived from the 3-dimensional structure from Brookhaven Protein Data Bank] + SwissProt =[Last major release of the SWISS-PROT protein sequence database (no updates)] + PIR + PRF)
- b. Limit by entrez query: No limitations were made which means all subsets of the above-cited databases were searched without any exclusions.
- c. Filter used: Low complexity. Filtering can eliminate statistically significant but biologically uninteresting reports from the blast output (e.g., hits against common acidic-, basic- or proline-rich regions), leaving the more biologically interesting regions of the query sequence available for specific matching against database sequences. Furthermore, in some cases, sequences are masked in their entirety,

Appl. No. 09/647,377

indicating that the statistical significance of any matches reported against the unfiltered query sequence should be suspect.

- d. Expect value = 10. This is the statistical significance threshold for reporting matches against database sequences. When the default value is 10, only 10 matches are expected to be found merely by chance, according to the stochastic model of Karlin and Altschul (1990). If the statistical significance ascribed to a match is greater than the EXPECT threshold, the match will not be reported. Lower EXPECT thresholds are more stringent, leading to fewer chance matches being reported. Increasing the threshold shows less stringent matches. Fractional values are acceptable.
- e. Word size = 3. This sets the size of the short regions of similarity between sequences for which BLAST initially searches.
- f. Matrix = BLOSUM62; Gap Costs: Existence = 11; Extension = 1. Here, the theory of amino acid substitution matrices is described in [1], and applied to DNA sequence comparison in [2]. In general, different substitution matrices are tailored to detecting similarities among sequences that are diverged by differing degrees [1-3]. A single matrix may nevertheless be reasonably efficient over a relatively broad range of evolutionary change [1-3]. Experimentation has shown that the BLOSUM-62 matrix [4] is among the best for detecting most weak protein similarities. For particularly long and weak alignments, the BLOSUM-45 matrix may prove superior. A detailed statistical theory for gapped alignments has not been developed, and the best gap costs to use with a given substitution matrix are determined empirically.

[1] Fitch, W.M. (1983) "Random sequences." *J. Mol. Biol.* 163:171-176

[2] Lipman, D.J., Wilbur, W.J., Smith T.F. & Waterman, M.S. (1984) "On the statistical significance of nucleic acid similarities." *Nucl. Acids Res.* 12:215-226.

[3] Altschul, S.F. & Erickson, B.W. (1985) "Significance of nucleotide sequence alignments: a method for random sequence permutation that preserves dinucleotide and codon usage." *Mol. Biol. Evol.* 2:526-538.

Appl. No. 09/647,377

[4] Dekker, J. (1983) "Probabilistic behavior of longest-common-subsequence length." In "Time Warps, String Edits and Macromolecules: The Theory and Practice of Sequence Comparison." D. Sankoff & J.B. Kruskal (eds.), pp. 55-91, Addison-Wesley, Reading, MA.

NCBI Blast searches have for years been a routine and standard tool used by scientists for identifying similarities between sequences. The following citation from NCBI (http://www.ncbi.nlm.nih.gov/BLAST/blast_overview.html) attests to this fact: "*BLAST® (Basic Local Alignment Search Tool) is a set of similarity search programs designed to explore all of the available sequence databases regardless of whether the query is protein or DNA. The BLAST programs have been designed for speed, with a minimal sacrifice of sensitivity to distant sequence relationships. The scores assigned in a BLAST search have a well-defined statistical interpretation, making real matches easier to distinguish from random background hits. BLAST uses a heuristic algorithm which seeks local as opposed to global alignments and is therefore able to detect relationships among sequences which share only isolated regions of similarity.*"

Using the above described standard blast procedure and SEQ ID No.: 9 of the present invention as a query, I obtained the following results: The hit showing the highest degree of identity in the blastP search performed was database identification No gi 25019857 (accession XP_110318.2). This protein is identified as being similar to hypothetical protein MGC37640 from *Mus musculus* and had a 97% sequence identity and a 97% sequence similarity. The murine LOBO protein of the present invention and XP_110318.2 lack identity for only 16 amino acid residues. This is likely the result of, for example, irresolvable secondary structure encountered during the sequencing process. Based on this alignment, I believe that XP_110318.2 and SEQ ID No. 9 describe one and the same sequence having equivalent functions. The nine other hits having a degree of identity greater than 70% are listed in Table 1. All of these proteins were of human or mouse origin. While the identity values for the last three sequences listed in Table 1 (Accession Nos. BAC03400.1, AAH30113.1 and XP_237349.1) have sequence identities ranging from 88% to 91%, these sequences represent a comparison of only 128-188 amino acids of the query sequences.

Appl. No. 09/647,377

The results of the blastP search are ordered by the value of % identity (see Table 2). The next "best" hit, after the 10 noted above, in the blastP search showed 37% identity to the protein sequence of SEQ ID NO.: 9. This next best hit in the blastP search has the identification No. gi 21292324 (equal to accession number EAA04469.1), which is defined as agCP3212 [*Anopheles gambiae* str. PEST]. The alignment of the polypeptide translated from gi 21292324 with SEQ ID NO.: 9 resulted in the value of 37% identity and accounted for 794 amino acid residues. In conclusion there are no proteins appearing in the blastP search having more than 70% identity to the amino acid sequence of SEQ ID NO.: 9 (murine LOBO protein).

All of the closest hits obtained in the blastP search, as identified in Table 1, were entered into the BLAST database after the filing date of the above-identified application. Furthermore, no function has been attributed to these sequences as illustrated by their descriptions, i.e. "hypothetical protein", etc. I believe that these proteins will have the same basic function as the murine LOBO protein given the significant degree of sequence identity and sequence similarity.

The undersigned hereby declares that all statements made herein based upon knowledge are true, and that all statements made based upon information and belief are believed to be true; and further, that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

DATED:

Feb - 27 - 2003Andreas Rumpf

Dr. Andreas Rumpf

Enclosures: As stated above



4# to #15

*Dr. Andreas Rump
Curriculum vitae*

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Personal Details

- Date of birth: **Sept. 7, 1960**
- Place of birth: **Hamm, Germany**
- Nationality: **German**
- Family status: **married, 5 children**
- **Private Address:**
Andreas Rump, Leutraer Weg 3a, 07745 Jena
☎ +49-3641-212866
✉ andreas_rump@hotmail.com

Current place of work

• **Since December 2000**

Employed at *metaGen Pharmaceuticals*, a company dedicated to the identification of potential targets suitable for the treatment of solid tumors. Position: Scientific Leader of the "genomic technologies group"; involved in large-scale annotation of genomic DNA, cloning and expression of full-length cDNAs, DNA sequence analysis and early validation of target genes.

Previous places of work

• **January 1996 - November 2000 (5 years)**

Research Scientist at the *Institute of Molecular Biotechnology* (IMB), *Dept. of Genome Analysis*, headed by Prof. Dr. André Rosenthal. Areas of work: large-scale sequencing and molecular characterization of mouse mutants with defects in bone development.

• **July 1994 -December 1995 (1.5 years)**

PostDoc at the *Institute of Neuropathology* in Heidelberg, headed by Prof. Dr. Marika Kiessling. Area of work: expression of glutamate receptors after global cerebral ischemia.

- **July 1991 – June 1994 (3 years)**

PostDoc at the *German Cancer Research Center* (DKFZ) in Heidelberg.

Department: „Interactions of carcinogens with biological macromolecules“, headed by Prof. Dr. Dr. Heinz-Walter Thielmann.

Area of work: molecular characterization of the basal cell nevus syndrome.

Postgraduate education

- **July 1987 – June 1991 (4 years)**

Ph.D. student within the *Dept. of Molecular Genetics*, at the German *National Research Center for Environment and Health* (GSF).

Ph.D. thesis: "Molecular characterization of the pythopathogenic fungus *Phytophthora parasitica*: construction of a representative genomic cosmid library and identification of pathologically relevant genes".

Undergraduate education

- **October 1980 – June 1987 (7 years)**

Student at the Institute of Biology at the University of Bielefeld, Germany. Diploma thesis from the *Dept. of Molecular Biology and Genetics*, headed by Prof. Dr. Alfred Pühler. Title of thesis: "Nucleotide sequence of the *nifA* gene of *Klebsiella pneumoniae* M5a1".

Berlin, Feb. 21, 2003

Andreas Rump

Publications

Gene 295 (2002) 27-32

Different structural organization of the encephalopsin gene in man and mouse

Kasper G, Taudien S, Staub E, Mennerich D, Rieder M, Hinzmann B, Dahl E, Schwidetzky U, Rosenthal A, **Rump A**.

Biochem Biophys Res Comm 289 (2001) 1287-1294

Gene structure and regulation of the murine epithelial calcium channels ECaC1 and 2

Weber K, Erben RG, **Rump A**, Adamski J.

Genomics 78 (2001) 197-205

A high-resolution genetic, physical, and comparative gene map of the doublefoot (Dbf) region of mouse chromosome 1 and the region of conserved synteny on human chromosome 2q35

Hayes C, **Rump A** (shared 1st authorship), Cadman MR, Harrison M, Evans EP, Lyon MF, Morriss-Kay GM, Rosenthal A, Brown SD.

Genomics 73 (2001) 55-55

Complex arrangement of genes within a 220-kb region of double-duplicated DNA on human 2q37.1

Rump A, Kasper G, Hayes C, Wen G, Starke H, Liehr T, Lehmann R, Lagemann D, Rosenthal A.

Nature 409 (2001) 860-921

Initial sequencing and analysis of the human genome

Author list from IMB Jena: Rosenthal A, Platzer M, Nyakatura G, Taudien S, **Rump A**.

Trends in Genetics 16 (2000) 519-520

RUMMAGE – a high throughput sequence annotation system

Taudien S, **Rump A**, Platzer M, Drescher B, Schattevoy R, Gloeckner G, Dette M, Baumgart C, Weber J, Menzel U, Rosenthal A.

Cytogenet Cell Genet 91 (2000) 224-230

Elevated DNA sequence diversity in the genomic region of the phosphatase PPP2R3L gene in the human pseudoautosomal region

Schiebel S, Meder J, **Rump A**, Rosenthal A, Winkelmann W, Fischer C, Rappold GA.

Genome Res 10 (2000) 758-775

Comparative genome sequence analysis of the Bpa/Str region in mouse and Man

Mallon AM, Platzer M, Bate R, Gloeckner G, Botcherby MR, Nordsiek G, Strivens MA, Kioschis P, Dangel A, Cunningham D, Straw RN, Weston P, Gilbert M, Fernando S, Goodall K, Hunter G, Greystong JS, Clarke D, Kimberley C, Goerdes M, Blechschmidt K, **Rump A**, Hinzmann B, Mundy CR, Miller W, Poustka A, Herman GE, Rhodes M, Denny P, Rosenthal A, Brown SD.

Nature 405 (2000) 311-319

The DNA sequence of human chromosome 21. The chromosome 21 mapping and sequencing consortium

Hattori M, Fujiyama A, Taylor TD, Watanabe H, Yada T, Park HS, Toyoda A, Ishii K, Totoki Y, Choi DK, Soeda E, Ohki M, Takagi T, Sakaki Y, Taudien S, Blechschmidt K, Polley A, Menzel U, Delabar J, Kumpf K, Lehmann R, Patterson D, Reichwald K, **Rump A**, Schillhabel M, Schudy A. et al.

Nat Genet. 16 (1997) 54-63

Pseudoautosomal deletions encompassing a novel homeobox gene cause growth failure in idiopathic short stature and Turner syndrome

Rao E, Weiss B, Fukami M, **Rump A**, Niesler B, Mertz A, Muroya K, Binder G, Kirsch S, Winkelmann M, Nordsiek G, Heinrich U, Breuning MH, Ranke MB, Rosenthal A, Ogata T, Rappold GA.

J Cereb Blood Flow Metab 16 (1996) 1362-1365

Editing of GluR2 RNA in the gerbil hippocampus after global cerebral ischemia

Rump A, Sommer C, Gass P, Bele S, Meissner D, Kiessling M.

Arch Dermatol Res. 288 (1996) 399-401

Basal cell nevus syndrome and dysplastic nevus syndrome: investigation of gene expression by differential hybridisation

Rump A, Fleischmann P, Jung EG, Werner D, Thielmann HW.

Gene 102 (1991) 51-56

Tandem arrangement of tRNA(Asp)-encoding genes in *Phytophthora* spp.

Rump A, Karlovsky P.

J Mol Biol 203 (1988) 715-738

Nucleotide sequence of a 24,206-base-pair DNA fragment carrying the entire nitrogen fixation gene cluster of *Klebsiella pneumoniae*

Arnold W, Rump A, Klipp W, Priefer UB, Pühler A.

APPENDIX I

LOBO coding sequence (CDS)-alignment: Mouse (complete) vs. Man (partial, as known at the time of patent filing)
 Region of overlap 1521 nt; Identiy [:] 85.2 %
 Program used: LALIGN (rigorous local alignment)

1120	1130	1140	1150	1160	1170
MM-LOB	AAAGACTGTATCTTCACCATTGATCCATCAACTGCTCGCGACCTTGATGCCCTGCC				

HS-Lob	AAAGACTGTATCTTCACCATTGACCCATCAACCGCCCGAGACCTCGATGCCCTCTCC				

10	20	30	40	50	60
1180	1190	1200	1210	1220	1230
MM-LOB	TGCAGGCAGGCTCACTGATGGCACCTTCAAGTGGCGTCCACATGCCGATGTGAGTTAC				

HS-Lob	TGCAAGCCACTCGCTGACGGCAACTCAAAGTGGAGTTCACATTGCTGACGTGAGTTAC				

70	80	90	100	110	120
1240	1250	1260	1270	1280	1290
MM-LOB	TTTGTTCCTGAGGGATCCTCTTGGATAAAGTAGCTGCTGAGAGAGGCCACAAGTGTCTAC				

HS-Lob	TTTGTTCGGAGGGATCTGATCTGGATAAAGTGGCTGCCAGAGGGCTACAAGCGTCTAC				

130	140	150	160	170	180
1300	1310	1320	1330	1340	1350
MM-LOB	TTGGTCCAGAACGGTGGCCCCATGCTTCCCAGGCTTGTGAGGAACCTGCAGCCTC				

HS-Lob	TTGGTTCAAAAGGTGGTCCCCATGCTTCCCAGGCTGCTGTGAGGAGCTGTGCAGCCTC				

190	200	210	220	230	240
1360	1370	1380	1390	1400	1410
MM-LOB	AACCCCATGACTGACAAGCTGACCTTCTGTGATCTGGAAAGCTGACCCCTGAAGGCAAG				

HS-Lob	AACCCCATGTCCGACAAGCTGACCTTCTGTGATCTGGACACTGACTCCAGAGGGCAAG				

250	260	270	280	290	300
1420	1430	1440	1450	1460	1470
MM-LOB	ATCCTTGAAGAGTGGTTGGCCGCACTATCATCCGTTCTGCACCAAACGTGAGCTACGAC				

HS-Lob	ATCCTTGAATGGTTGGCCGGACCATCATCCGCTCTGCACCAAACCTAGCTACGAG				

310	320	330	340	350	360
1480	1490	1500	1510	1520	1530
MM-LOB	CATGCCAGAGCATGATCGAAAATCCAACGTGAGAAGATCCCTGAGGAAGAGCTTCCCCA				

HS-Lob	CATGCACAGAGCATGATTGAAAGCCCAACTGAGAAAATCCCTGCGAAAGAGCTGCCCCC				

370	380	390	400	410	420
1540	1550	1560	1570	1580	1590
MM-LOB	ATTTCTCCAGAGCACAGCGTCGAGGAGGTGCACCGAGCAGTCCTGAACCTGCACAGCATT				

HS-Lob	ATTTCCCCAGAGCATAGCAGCGAGGAGGTACACCAGGCCGTCTGAATCTCACCGAATT				

430	440	450	460	470	480
1600	1610	1620	1630	1640	1650
MM-LOB	GCAAAGCAAATCCGCCGCCAGCGCTTGTAGATGGCGCACTCCGTTAGATCAGCTGAAG				

HS-Lob	GCCAAGCAGTTACGCCAGCAGCGCTTGTGGACGGCGACTTCGTTGGATCAGCTAAAG				

490	500	510	520	530	540

1660	1670	1680	1690	1700	1710
MM-LOB	CTTGCTTTACTCTGGACCATGAGACTGGACTGCCTCAAGGATGTACATCTATGAGTAC				

HS-Lob	CTTGCTTCACTCTGGACCACGAGACCGATTGCCTCAAGGATGTACATCTATGAGTAC				
	550	560	570	580	590
	600				
1720	1730	1740	1750	1760	1770
MM-LOB	CGAGACAGCAACAAGCTTAGAGGAGTTCATGCTCCTGGCCAACATGGCGGTGGCCAC				

HS-Lob	CGCGAGAGCAACAAGCTCGTGGAGGAGTTCATGCTCTGGCCAACATGGCAGTGGCCAC				
	610	620	630	640	650
	660				
1780	1790	1800	1810	1820	1830
MM-LOB	AAGATCTCCGCACCTCCCTGAGCAGGCCCTGCTGCGCCGGCATCCCCAACACAGACG				

HS-Lob	AAGATCCACCGCGCCTCCCCGAGCAGGCCCTGCTGCGCCGGCACCCCCGCCAAACA				
	670	680	690	700	710
	720				
1840	1850	1860	1870	1880	1890
MM-LOB	AAGATGCTCAGTGACCTGGTGGAGTTCTGTGACCAGATGGGCTGCCATGGATGTCAGC				

HS-Lob	AGGATGCTCAGTGACCTGGTGGAATTCTGCGACCAGATGGGCTGCCGTGGACTTCAGC				
	730	740	750	760	770
	780				
1900	1910	1920	1930	1940	1950
MM-LOB	TCTGCAGGGCCCTAAATAAAAGCCTGACTAAGACATTGGAGATGACAAGTACTCTG				

HS-Lob	TCCGCAGGAGCCCTCAATAAAAGCCTGACCCAAACATTGGAGATGACAAGTACTCACTG				
	790	800	810	820	830
	840				
1960	1970	1980	1990	2000	2010
MM-LOB	GCCCCGAAGGAGGTGCTCACCAACATGTACTCCGCCCATGCAGATGGCACTGTACTTC				

HS-Lob	GCCCCGAAGGAGGTGCTCACCAACATGTGCTCCGCCCATGCAGATGGCACTGTACTTC				
	850	860	870	880	890
	900				
2020	2030	2040	2050	2060	2070
MM-LOB	TGCTCTGGATGCTGCAGGACCAGGAGCAGTCCGGCATTATGCTCTAACGTTCCCCTC				

HS-Lob	TGCTCGGGCTGCTGCAGGACCCAGCGCAGTCCGGCACTACGCGCTCAATGTGCCCTG				
	910	920	930	940	950
	960				
2080	2090	2100	2110	2120	2130
MM-LOB	TACACACACTTCACCTCTCCCATCCGCCGTTGCTGACGTACAGTCACCGCCTCTG				

HS-Lob	TACACACACTTCACCTCGCCCATCCGCCGTTGCCGACGTCCGTGGTCACCGCCTCTG				
	970	980	990	1000	1010
	1020				
2140	2150	2160	2170	2180	2190
MM-LOB	GCTGCTGCTCTGGCTACAGTGAACAGCCAGATGTGGAGCCTGATAACCTACAGAACAA				

HS-Lob	GCTGCCCGTTAGGCTATAGGGAGCGACTAGACATGGGCCGATAACCTGCAGAACAG				
	1030	1040	1050	1060	1070
	1080				
2200	2210	2220	2230	2240	2250
MM-LOB	GCTGACCACTGCAATGACCGTCGCATGGCTCAAACGTGTGCAGGAGCTCAGCCTCGGC				

HS-Lob	CGGGACCACTGTAACGACCGCCGCATGGCGTCCAAGCGCGTGCAGGAGCTCAGTACAGT				

	1090	1100	1110	1120	1130	1140
	2260	2270	2280	2290	2300	2310
MM-LOB	CTCTTCTTCGCAGTTCTAGTAAAGGAGAGTGGCCCCCTGGAGTCCGAAGCCATGGTATG	:::::::	:::::	:::::::	:::::::	:::::::
HS-Lob	CTCTTCTTGCTGTTCTGGTCAAGGAGAGTGGCCCCCTGGAGTCAGAAGCCATGGTATG	1150	1160	1170	1180	1190
	1200					
	2320	2330	2340	2350	2360	2370
MM-LOB	GGTGTCTGAACCAAGCTTCGACGTGCTGGTGCTGCGCTTGGGTGCAGAACGCGCATC	::	:::::	:::::	:::::	:::::
HS-Lob	GGCATCCTGAAGCAAGCCTCGACGTGCTGGTGCTGCGCTACGGCGTGCAGAACGCGCATC	1210	1220	1230	1240	1250
	1260					
	2380	2390	2400	2410	2420	2430
MM-LOB	TACTGCAATGCACTGGCCCTGCGATCCTACAGCTTCCAGAACGGTGGGAAGAACGCCAGAG	:::::	:::::::::::	:::::	:::::::::::	:::::
HS-Lob	TACTGCAACGCACTGGCCCTCGGGTCCCACCACTCCAGAACGGTGGCAAGAACGCCGAA	1270	1280	1290	1300	1310
	1320					
	2440	2450	2460	2470	2480	2490
MM-LOB	CTCACTCTGTTGGGAGCCTGATGACCTTGAAGAGGAGCCAACACAGCAGGTCACTCACC	:::::	:::	:::::	:::::	:::::
HS-Lob	CTCACGCTGGTCTGGGAGCCTGAGGACATGGAGCAGGAGCCACAGCAGGTCACTCACC	1330	1340	1350	1360	1370
	1380					
	2500	2510	2520	2530	2540	2550
MM-LOB	ATCTTCAGCCTGGTGGATGTGGTCCTGCAGGCAGAGGCCACAGCCCTCAAGTACAGTGCT	:::::::::::	:::::::::::	:::::::::::	:::::::::::	::
HS-Lob	ATCTTCAGCCTGGTGGAGGTGGTCCTGCAGGCAGAGTCCACAGCCCTCAAGTACAGCGCC	1390	1400	1410	1420	1430
	1440					
	2560	2570		2580		2590
MM-LOB	ATCCTGAAGCGACCAGGC-----CTGG-----AGAAGGCGTCT	::::::::::	:::::	::::	:: :: ::	
HS-Lob	ATCCTGAAGCGGCCAGGCACCCAGGGCACCTGGGCCCTGAGAACGGAGGAGGAGTCT	1450	1460	1470	1480	1490
	1500					
	2600	2610				
MM-LOB	GATGAGGAGCCTGAGGACTGA	:: :	:::::	:::::		
HS-Lob	GACGGTGAGCCCGAGGACTCA	1510	1520			

LOBO Protein-Alignment: Mouse (complete) vs. Man (partial, as known at the time of patent filing)

Region of overlap 506 aa; Identiy [:] 88.1 %; Similarity [.] 94.8 %

Program used: LALIGN (rigorous local alignment)

380	390	400	410	420	430
MM-LOB	KDCIFTIDPSTARLDALACRRLTDGTFEVGVHIADVSYFPEGSSLDKVAERATSVY				

HS-LOB	KDCIFTIDPSTARLDALSKPLADGNFKVGVHIADVSYFPEGSDLDKVAERATSVY				

10	20	30	40	50	60
440	450	460	470	480	490
MM-LOB	LVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPEGKILEEWFGR T IIRSCTKLSYD				

HS-LOB	LVQKVVPMLPRLLCEELCSLNPMSDKLTFSVIWTLTPEGKILDEEWFGR T IIRSCTKLSYE				

70	80	90	100	110	120
500	510	520	530	540	550
MM-LOB	HAQSMIENPTEKIPPEELPPISPEHSVEEVHQAVLNLSIAKQLRRQRFVDGALRLDQLK				

HS-LOB	HAQSMIESPTEKIPAKELPPISPEHSSEEVHQAVLNHGIAKQLRQQRFVDGALRLDQLK				

130	140	150	160	170	180
560	570	580	590	600	610
MM-LOB	LAFTLDHETGLPQGCHIYEYRDSNKLVEEFMILLANMAVAHKIFRTFPEQALLRRHPPPQT				

HS-LOB	LAFTLDHETGLPQGCHIYEYRESNKLVEEFMILLANMAVAHKIHRAFPEQALLRRHPPPQT				

190	200	210	220	230	240
620	630	640	650	660	670
MM-LOB	KMLSDLVEFC DQMGLPMDVSSAGALNKSLTKTFGDDKYSLARKEVLTNMYSRPMQMALYF				

HS-LOB	RMLSDLVEFC DQMGLPVDFSSAGALNKSLTQTFGDDKYSLARKEVLTNMCSRPMQMALYF				

250	260	270	280	290	300
680	690	700	710	720	730
MM-LOB	CSGML DQEFRHYALNVPLYTHFTSPIRFA DVIVHRL LAAALGYSEQPDVEPDTLQKQ				

HS-LOB	CSG LLQDPAQFRHYALNVPLYTHFTSPIRFA DVLVHRL LAAALGYRERLDMAPDTLQKQ				

310	320	330	340	350	360
740	750	760	770	780	790
MM-LOB	ADHC NDRRMASKRVQELSIGLFFAVLVKE SGPLESEAMVMGVLNQAFDVLVLRFGVQKRI				

HS-LOB	ADHC NDRRMASKRVQELSTSLFFAVLVKE SGPLESEAMVMGILKQAFDVLVLYGVQKRI				

370	380	390	400	410	420
800	810	820	830	840	850
MM-LOB	YCNALALRSYS FQKVGGKKPE TLWEPDDLEEEPTQQVITIFSLVDVVLQAEATALKYSA				

HS-LOB	YCNALALRS HFQKVGGKKPE TLWEPEDMEQEPAQQVITIFSLVEVVLQAEESTALKYSA				

430	440	450	460	470	480
860		870			
MM-LOB	ILKRPGL-----EKASDEEPE D				

HS-LOB	ILKRP GTQGHLGPEKEEEE SDGEPE D				

490	500				

APPENDIX II

LOBO Protein-Alignment: Mouse (complete) vs. Man (complete, as determined after patent filing)

Region of overlap 881 aa; Identiy [:] 88.3 %; Similarity [.] 96.2 %

Program used: LALIGN (rigorous local alignment)

10	20	30	40	50	60
MM-LOB MNHPDYKLNLRSPGTPRGVSSVVGPSAVGASPGDKSKNKS MRGKKKSIFETYMSKEDVS
HS-LOB MSHPDYRMNLRLPLGTPRGVSAVAGPHIDIGASPGDKSKNRSTRGKKKSIFETYMSKEDVS
10	20	30	40	50	60
70	80	90	100	110	120
MM-LOB EGLKRGTLIQQVLRINPKKFHEAFIPS PGDRDIFIDGVVAR NRALNGDLVVVKLLPEDQ
HS-LOB EGLKRGTLIQQVLRINPKKFHEAFIPS PGDRDIFIDGVVAR NRALNGDLVVVKLLPEEH
70	80	90	100	110	120
130	140	150	160	170	
MM-LOB WKAVKPESNDKEIEATYEADIP EEGCGHHPLQQSRKGWS-GPDVIIEAQFDDSDSEDRHG
HS-LOB WKVVKPESNDKETEAAYESDIPEELCGHHLPQQSLKSY NDSPDVIV EAQFDGSDSEDGHG
130	140	150	160	170	180
180	190	200	210	220	230
MM-LOB NTSG-LVDGVKKL SISTPDRGKEDSSTPVMKDENTPI PQDTRGLSEKSLQSAKVYYILE
HS-LOB ITQNVLV DGVKKL SVCSEKGREDGDAPVTKDETTCIS QDTRALSEKSLQRSAKVYYILE
190	200	210	220	230	240
240	250	260	270	280	290
MM-LOB KKHSRAATGILKLLADKNSDLFKKYALFSP PSDHRVPRIYVPLKDCPQDFMTRPKDFANTL
HS-LOB KKHSRAATGFLKLLADKNSELFRKYALFSP PSDHRVPRIYVPLKDCPQDFVARPKDYANTL
250	260	270	280	290	300
300	310	320	330	340	350
MM-LOB FICRIIDWKEDCNFAL GQLAKSLGQAGEIEPETEGILTEYGVDFSD FSSEVLECLPQSLP
HS-LOB FICRIVDWKEDCNFAL GQLAKSLGQAGEIEPETEGILTEYGVDFSD FSSEVLECLPQGLP
310	320	330	340	350	360
360	370	380	390	400	410
MM-LOB WTIPPDEVGKRRDLRKDCIFTIDPSTAR DL DALACRRLTDGT FEVGVHIADVS YFVPEG
HS-LOB WTIPPEEFSKRRDLRKDCIFTIDPSTAR DL DALSKPLADGNFKVG VHIADVS YFVPEG
370	380	390	400	410	420
420	430	440	450	460	470
MM-LOB SS LDKVA AERAT SVYLVQ KV VPML PR LLCE ELCS LNP MTD KLT FS V IWK LT PEG KILE EW
HS-LOB SD LDKVA AERAT SVYLVQ KV VPML PR LLCE ELCS LNP MSDKLT FS V IWT LT PEG KIL DEW
430	440	450	460	470	480
480	490	500	510	520	530
MM-LOB FGRTII RSCTKLSYDHAQSMIENPTEKI PEEELPPISPEHSVEEVHQAVLN LHSIAKQLR
HS-LOB FGRTII RSCTKLSYEHAQSMIESPTEKI PAKELPPISPEHSSEE VHQA VLN LHGI AKQLR
490	500	510	520	530	540

540 550 560 570 580 590
MM-LOB RQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRT
.....
HS-LOB QQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRESNKLVEEFMLLANMAVAHKIHRA
550 560 570 580 590 600

600 610 620 630 640 650
MM-LOB FPEQALLRRHPPPQTCKMLSDLVEFCDCQMQGLPMVDSSAGALNKS LT KTFGDDKYSLARKEV
.....
HS-LOB FPEQALLRRHPPPQTCKMLSDLVEFCDCQMQGLPVDFSSAGALNKS LT QTFGDDKYSLARKEV
610 620 630 640 650 660

660 670 680 690 700 710
MM-LOB LTNMYSRPMQM ALYFCSGMLQDQE QFRHYALNVPLYTHFTSPIR RFAD VIVHRL LAA ALG
.....
HS-LOB LTNMCSRPMQM ALYFCSGLLQDPAQFRHYALNVPLYTHFTSPIR RFAD VLVHRL LAA ALG
670 680 690 700 710 720

720 730 740 750 760 770
MM-LOB YSEQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVLVKE SG PLESEAMVMGVLNQ
.....
HS-LOB YRERLDMA PDTLQKQADHCNDRRMASKRVQELSTSLFFAVLVKE SG PLESEAMVMGILKQ
730 740 750 760 770 780

780 790 800 810 820 830
MM-LOB AFDVLVLRFGVQKRIYCNALALRSYSFQKVGGKPELT LVWE PDDLEEPTQQVITIFSLV
.....
HS-LOB AFDVLVLRYGVQKRIYCNALALRSHHFQKVGGKPELT LVWE PEDMEQEP AQVITIFSLV
790 800 810 820 830 840

840 850 860 870
MM-LOB DVVLQAEATALKYSAILKRPGL-----EKASDEEPE D
.....
HS-LOB EVVLQAEESTALKYSAILKRPGTQGH LGPEKEEEE SDGEPE D
850 860 870 880

LOBO coding sequence (CDS)-alignment: Mouse (complete) vs. Man (complete, as determined after patent filing)
Region of overlap 2646 nt; Identiy [:] 85.9 %
Program used: LALIGN (rigorous local alignment)

	10	20	30	40	50	60
MM-LOB	ATGAACCACCTGACTACAAGCTGAACCTTCGGTCTCCGGGACCCCCAGAGGTGTGCC					
	::::::::::: ::::::::::: ::::::: :: : :::::::::::::::::::::					
HS-Lob	ATGAGCCACCTGACTACAGAACCTCCGGCCCTGGGGACCCCCAGAGGTGTCT					
	10	20	30	40	50	60
	70	80	90	100	110	120
MM-LOB	TCTGTGGTTGGCCCGAGTGCTGTTGGTCTCGCCAGGTGACAAAAGTCAAAGAACAG					
	::::::: ::::: :: : ::::::::::::::::::::: :::::::::::::::::::::					
HS-Lob	GCTGTGGCTGGTCCACATGACATTGGTGCTTCGCCAGGTGACAAAAGTCAAAGAACAGG					
	70	80	90	100	110	120
	130	140	150	160	170	180
MM-LOB	TCCATGCGAGGGAAGAAAAAGAGCATATTGAAACCTACATGTCCAAGGAGGATGTTCA					
	::::: ::::::::::::::::::::: ::::::::::::::::::::: :::::::::::::::::::::					
HS-Lob	TCCACACGAGGGAAGAAAAAGAGCATATTGAAACTACATGTCCAAGGAGGATGTTCA					
	130	140	150	160	170	180
	190	200	210	220	230	240
MM-LOB	GAAGGCTTGAAGAGAGGAACACTTATCCAGGGTGTATTGAGAATCAACCCAAAGAAGTT					
	::::::: ::::::::::::::::::::: ::::::::::::::::::::: :: :: :: :: :: :: ::					
HS-Lob	GAAGGCTTGAAGAGAGGAACACTCATCCAGGGTGTATTGAGAATTAAATCCAAAGAAGTT					
	190	200	210	220	230	240
	250	260	270	280	290	300
MM-LOB	CATGAAGCCTTCATTCTTCTCCGGATGGTGTACGGGACATTATTGATGGAGTTGTT					
	::::::: ::::::::::::::::::::: ::::::::::::::::::::: :: :: :: :: :: ::					
HS-Lob	CATGAAGCCTTCATTCTTCCCCGGATGGTGTACGAGACATTATTGATGGGTTGTT					
	250	260	270	280	290	300
	310	320	330	340	350	360
MM-LOB	GCTCGTAATAGAGCCTTAAATGGGGACCTTGTGGTTGTAAAAGTCTCCTGAGGATCAG					
	::::::: ::::::::::::::::::::: :: :: :: :: :: :: :: :: :: :: :: ::					
HS-Lob	GCTCGTAATAGAGCCTTAAATGGGGATCTGGTGGTGTGAAACTGCTCCGAGGAGCAT					
	310	320	330	340	350	360
	370	380	390	400	410	420
MM-LOB	TGGAAGGCAGTTAACCAACAGAGAGCAATGACAAAGAAATAGAAGCTACTTATGAAGCTGAC					
	::::::: ::::::::::::::::::::: :: :: :: :: :: :: :: :: :: :: ::					
HS-Lob	TGGAAGGTAGTTAACCAACAGAGAGCAATGACAAAGAAACAGAAGCTGCGTATGAATCAGAT					
	370	380	390	400	410	420
	430	440	450	460	470	
MM-LOB	ATCCCTGAAGAGGGCTGTGGACATCACCCCTGCAGCAGTCCGGAAAGGCTGGAGTG--					
	::::: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::					
HS-Lob	ATCCCCGAGGAGCTCTGTGGACACCATCTCCGCAACAGTCCCTGAAAAGCTATAATGAC					
	430	440	450	460	470	480
	480	490	500	510	520	530
MM-LOB	-GTCCTGATGTCATTATAGAGGCTCAGTTGATGACAGCGACTCAGAAGATAGACATGGC					
	::::::: ::::::::::::::::::::: :: :: :: :: :: :: :: :: :: :: ::					
HS-Lob	AGTCCTGATGTCATTGTAGAGGCTCAGTTGATGGCAGCGACTCAGAAGATGGACATGGC					
	490	500	510	520	530	540

540	550	560	570	580	590
MM-LOB	AACACC---	AGTGGCCTGGTTGATGGTGTAAAGAAATTGTCAATCTACTCCTGACAGA			
: :	: :	: :	: :	: :	: :
HS-Lob	ATCACACACAAATGTGCTGGTTGATGGTGTAAAGAAACTCTCAGTTGTGTTCTGAGAAA				
550	560	570	580	590	600
600	610	620	630	640	650
MM-LOB	GGAAAAGAAGATTCTAGTACTCCAGTTATGAAAGATGAGAACACCCCCATACCACAGGAC				
: :	: :	: :	: :	: :	: :
HS-Lob	GGAAGAGAGGGATGGTGATGCACCGGTACAAAAGATGAGACCACCTGCATTCACAAGAC				
610	620	630	640	650	660
660	670	680	690	700	710
MM-LOB	ACAAGAGGGCTTATCAGAGAAGTCACTCAGAAATCAGCAAAGGTGGTTACATCTTGGAG				
: :	: :	: :	: :	: :	: :
HS-Lob	ACAAGAGCTTATCGGAGAAATCCCTGCAAAGATCAGCAAAGGTGGTTACATCTTGGAG				
670	680	690	700	710	720
720	730	740	750	760	770
MM-LOB	AAAAAGCATTCTCGAGCAGCACTGGCATCCTGAAACTCTTGGCTGATAAGAACAGTGAC				
: :	: :	: :	: :	: :	: :
HS-Lob	AAAAAACATTCTCGAGCAGCAACCGGCTCCTCAAACCTCTTGGCTGATAAGAACAGCGAA				
730	740	750	760	770	780
780	790	800	810	820	830
MM-LOB	CTGTTAAGAAATACGCCCTGTTTCTCCTTCAGACCACCGAGTACCTAGAATTACGTA				
: :	: :	: :	: :	: :	: :
HS-Lob	CTGTTAGGAAATACGCCCTGTTTCTCCTTCAGACCACCGAGTGCCTAGAATTATGTG				
790	800	810	820	830	840
840	850	860	870	880	890
MM-LOB	CCTCTCAAGGACTGTCCCCAGGACTTCATGACCCGACCTAAAGACTTTGCCAACACGCTG				
: :	: :	: :	: :	: :	: :
HS-Lob	CCTCTCAAGGACTGTCCCCAGGACTTTGTGGCACGGCCTAAAGATTATGCCAACACACTG				
850	860	870	880	890	900
900	910	920	930	940	950
MM-LOB	TTCATCTGCCGCATCATAGACTGGAAGGAGGACTGTAATTTCGCCCTGGGGCAACTGGCT				
: :	: :	: :	: :	: :	: :
HS-Lob	TTCATCTGCCGCATTGTGGACTGGAAGGAGGACTGCAATTTCGCCCTGGGGCAGCTGGCT				
910	920	930	940	950	960
960	970	980	990	1000	1010
MM-LOB	AAGAGTCTGGCAGGCTGGTGAAATCGAGCCTGAAACAGAAGGGATACTGACAGAAATAT				
: :	: :	: :	: :	: :	: :
HS-Lob	AAGAGTCTGGCAGGCTGGTGAAATTGAGCCTGAAACAGAAGGAATACTAACAGAGTAT				
970	980	990	1000	1010	1020
1020	1030	1040	1050	1060	1070
MM-LOB	GGTGTGGACTTCTCTGATTCTCTCAGAAGTTCTGAAATGTCTCCCTCAAAGCCTGCC				
: :	: :	: :	: :	: :	: :
HS-Lob	GGCGTGGATTCTCTGATTCTCTCAGAAGTTCTAGAATGTCTCCCTCAAGGCCTGCCA				
1030	1040	1050	1060	1070	1080

	1080	1090	1100	1110	1120	1130
MM-LOB	TGGACAATCCCACCTGATGAGGTGGCAAGAGAAGAGACCTAAGGAAAGACTGTATCTC ::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::					
HS-Lob	TGGACAATTCCACCAGAGGAGTTCAGCAAGAGAAGGGATTAAGAAAAGACTGTATCTC 1090 1100 1110 1120 1130 1140					
	1140	1150	1160	1170	1180	1190
MM-LOB	ACCATTGATCCATCAACTGCTCGCACCTGATGATGCCCTCGCCTGCAGGCGGCTCACT ::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::					
HS-Lob	ACCATTGACCATCAACCGCCCGAGACCTCGATGATGCCCTCTCCTGCAAGGCCACTCGC 1150 1160 1170 1180 1190 1200					
	1200	1210	1220	1230	1240	1250
MM-LOB	GATGGCACCTTCGAAGTGGCGTCCACATGCCGATGTGAGTTACTTGTTCCCTGAGGGA ::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::					
HS-Lob	GACGGCAACTCAAAGTGGAGTTCACATTGCTGACGTGAGTTACTTGTTCCGGAGGGA 1210 1220 1230 1240 1250 1260					
	1260	1270	1280	1290	1300	1310
MM-LOB	TCCTCTTGGATAAAAGTAGCTGCTGAGAGAGGCCACAAGTGTACTTGGTCCAGAAGGTG ::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::					
HS-Lob	TCTGATCTGGATAAAAGTGGCTGCCGAGAGGGCTACAAGCGTCTACTTGGTTCAAAAGGTG 1270 1280 1290 1300 1310 1320					
	1320	1330	1340	1350	1360	1370
MM-LOB	GTCCCCATGCTTCCCAGGCTTCTGTGTGAGGAACCTGCAAGCCTCAACCCCATGACTGAC ::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::					
HS-Lob	GTCCCCATGCTTCCCAGGCTGCTGTGTGAGGAGCTGTGCAGCCTCAACCCCATGTCCGAC 1330 1340 1350 1360 1370 1380					
	1380	1390	1400	1410	1420	1430
MM-LOB	AAGCTGACCTTCTGTGATCTGGAAAGCTGACCCCTGAAGGCAAGATCCTGAAGAGTGG ::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::					
HS-Lob	AAGCTGACCTTCTGTGATCTGGACACTGACTCCAGAGGGCAAGATCCTGATGAATGG 1390 1400 1410 1420 1430 1440					
	1440	1450	1460	1470	1480	1490
MM-LOB	TTTGGCCGCACTATCATCCGTTCTGCACCAAACCTGAGCTACGACCATGCCAGAGCATG ::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::					
HS-Lob	TTTGGCCGGACCATCATCCGCTCTGCACCAAACCTAGCTACGAGCATGCACAGAGCATG 1450 1460 1470 1480 1490 1500					
	1500	1510	1520	1530	1540	1550
MM-LOB	ATCGAAAATCCAAC TGAGAAGATCCCTGAGGAAGAGCTTCCCCAATTCTCCAGAGCAC ::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::					
HS-Lob	ATTGAAAAGCCCAACTGAGAAAATCCCTGCGAAAGAGCTGCCCTTCCCCAGAGCAT 1510 1520 1530 1540 1550 1560					
	1560	1570	1580	1590	1600	1610
MM-LOB	AGCGTCGAGGAGGTGCACCAGGCAGTCCTGAACCTGCACAGCATTGCAAAGCAACTCCGC ::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::					
HS-Lob	AGCAGCGAGGAGGTACACCAGGCCGTCTGAATCTCACGGAATTGCCAAGCAGTTACGC 1570 1580 1590 1600 1610 1620					
	1620	1630	1640	1650	1660	1670
MM-LOB	CGCCAGCGCTTGTAGATGGCGCACTCCGTTAGATCAGCTGAAGCTGCTTTACTCTG ::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::					
HS-Lob	CAGCAGCGCTTGTGGACGGCGCACTCGTTGGATCAGCTAAAGCTGCTTCACTCTG 1630 1640 1650 1660 1670 1680					

1680	1690	1700	1710	1720	1730
MM-LOB	GACCATGAGACTGGACTGCCTCAAGGATGTCACATCTATGAGTACCGAGACAGCAACAAG				

HS-Lob	GACCACGAGACCGGATTGCCTCAAGGATGTCATATCTATGAGTACCGAGAGCAACAAG				
	1690	1700	1710	1720	1730
	1740	1750	1760	1770	1780
MM-LOB	CTTGTAGAGGAGTTCATGCTCCTGGCCAACATGGCGGTGGCCCACAAGATCTCCGCACC				

HS-Lob	CTCGTGGAGGAGTTCATGCTCTTGGCCAACATGGCAGTGGCCCACAAGATCCACCGCGCC				
	1750	1760	1770	1780	1790
	1800	1810	1820	1830	1840
MM-LOB	TTCCCTGAGCAGGCCCTGCTGCGCCGGCATCCCCACACAGACGAAGATGCTCAGTGAC				

HS-Lob	TTCCCCGAGCAGGCCCTGCTGCGCCGGCACCCCCGCCAAACAAGGATGCTCAGTGAC				
	1810	1820	1830	1840	1850
	1860	1870	1880	1890	1900
MM-LOB	CTGGTGGAGTTCTGTGACCAGATGGGCTGCCATGGATGTCAGCTCTGCAGGGGCCCTA				

HS-Lob	CTGGTGGATTCTGCGACCAGATGGGCTGCCGTGGACTTCAGCTCCGCAGGAGCCCTC				
	1870	1880	1890	1900	1910
	1920	1930	1940	1950	1960
MM-LOB	AATAAAAGCCTGACTAAGACATTTGGAGATGACAAGTACTCTGGCCCGGAAGGAGGTG				

HS-Lob	AATAAAAGCCTGACCCAAACATTTGGAGATGACAAGTACTCACTGGCCCGAAGGAGGTG				
	1930	1940	1950	1960	1970
	1980	1990	2000	2010	2020
MM-LOB	CTCACCAACATGTACTCCGGCCCATGCAGATGGCACTGTACTTCTGCTCTGGATGCTG				

HS-Lob	CTCACCAACATGTGCTCCGGCCCATGCAGATGGCACTGTACTTCTGCTCGGGCTGCTG				
	1990	2000	2010	2020	2030
	2040	2050	2060	2070	2080
MM-LOB	CAGGACCAGGAGCAGTCCGGCATTATGCTCTAACGTTCCCTCTACACACACTTCACC				

HS-Lob	CAGGACCCAGCGCAGTCCGGCACTACGCGCTCAATGTGCCCTGTACACACACTTCACC				
	2050	2060	2070	2080	2090
	2100	2110	2120	2130	2140
MM-LOB	TCTCCCATCCGCCGCTTGCTGACGTAGTCACCGCCTCCTGGCTGCTCTGGC				

HS-Lob	TCGCCCATCCGCCGCTTGCCGACGTCCCTGGTCACCGCCTCCTGGCTGCCGCTTAGGC				
	2110	2120	2130	2140	2150
	2160	2170	2180	2190	2200
MM-LOB	TACAGTGAACAGCCAGATGTGGAGCCTGATACCCTACAGAACAGCAAGCTGACCACTGCAAT				

HS-Lob	TATAGGGAGCGACTAGACATGGCGCCGATACCCTGCAGAACAGGGGGACCACTGTAAC				
	2170	2180	2190	2200	2210
	2220				

2220 2230 2240 2250 2260 2270
MM-LOB GACCGTCGCATGGCTTCAAACGTGTGCAGGAGCTCAGCATCGGCCTCTTCGCAGTT
::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
HS-Lob GACCGCCGCATGGCGTCCAAGCGCGTGCAGGAGCTCAGTACCACTCTTCTTGCTGTT
2230 2240 2250 2260 2270 2280

2280 2290 2300 2310 2320 2330
MM-LOB CTAGTAAAGGAGAGTGGCCCCCTGGAGTCCGAAGCCATGGTATGGGTGTCTGAACCAA
::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
HS-Lob CTGGTCAAGGAGAGTGGCCCCCTGGAGTCAGAACCATGGTATGGCATCCTGAAGCAA
2290 2300 2310 2320 2330 2340

2340 2350 2360 2370 2380 2390
MM-LOB GCTTCGACGTGCTGGTGCTGCGCTTGGGGTGCAGAAGCGCATCTACTGCAATGCACTG
::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
HS-Lob GCCTTCGACGTGCTGGTGCTGCGCTACGGCGTGCAGAACGCGCATCTACTGCAACGCACTG
2350 2360 2370 2380 2390 2400

2400 2410 2420 2430 2440 2450
MM-LOB GCCCTGCGATCCTACAGCTTCCAGAACGGTGGGAAGAACGCCAGAGCTCACTCTTGTGG
::: ::::: ::: :: ::::: ::::: ::::: ::::: ::: :: :: :::
HS-Lob GCCCTGCGGTCCCACCCTCCAGAACGGTGGCAAGAACGCCGGAACTCACGCTGGTCTGG
2410 2420 2430 2440 2450 2460

2460 2470 2480 2490 2500 2510
MM-LOB GAGCCTGATGACCTTGAAGAGGGAGCCAACACAGCAGGTATCACCCTTCAGCCTGGT
::: ::::: ::: :: ::::: ::::: ::::: ::::: ::::: :::::
HS-Lob GAGCCTGAGGACATGGAGCAGGAGCCAGCACAGCAGGTATCACCCTTCAGCCTGGT
2470 2480 2490 2500 2510 2520

2520 2530 2540 2550 2560 2570
MM-LOB GATGTGGTCCTGCAGGCAGAGGCCACAGCCCTCAAGTACAGTGCTATCCTGAAGCGACCA
::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
HS-Lob GAGGTGGTCCTGCAGGCAGAGTCCACAGCCCTCAAGTACAGCGCCATCCTGAAGCGGCCA
2530 2540 2550 2560 2570 2580

2580 2590 2600
MM-LOB GGC-----CTGG-----AGAAGGCGTCTGATGAGGAGCCTGAG
::: ::::: ::::: ::::: ::::: ::::: :::::
HS-Lob GGCACCCAGGCCACCTGGCCCTGAGAACGGAGGAGGAGTCTGACGGTGAGCCGAG
2590 2600 2610 2620 2630 2640

2610
MM-LOB GACTGA
::: ::
HS-Lob GACTCA

TABLE 1

Blast of complete mouse LOBO protein against translated GenBank produced hits with significant similarity with the following DB-entries (Blast performed 30-Jan-2003):

All other matches were significantly lower than 70 % aa identity

RESULT: no entry with significant (i.e. >70 % aa identity) was older than May 2002 !!

Similarity	Accession	Entry date	Remark
818/870 (94%)	NP_705758.1	26-JAN-2003	
801/831 (96%)	BAC27292.1	05-DEC-2002	
720/772 (93%)	XP_129937.2	16-NOV-2002	version 1: 08-OCT-2002
647/663 (97%)	XP_110318.2	15-NOV-2002	version 1: 30-APR-2002
569/590 (96%)	BAC26549.1	05-DEC-2002	
451/532 (84%)	AAH36113.1	23-SEP-2002	
410/527 (77%)	BAC04324.1	15-JUL-2002	
167/188 (88%)	BAC03400.1	15-JUL-2002	
119/135 (88%)	AAH30113.1	20-MAY-2002	
117/128 (91%)	XP_237349.1	28-JAN-2003	

TABLE 2

The detailed Blast results are as follows:

BLASTP 2.2.5 [version from Nov-16-2002]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1043949663-07491-641

Query= MM-LOBO 871 bp PROT 6-NOV-1998,
871 bases, 670 checksum.
(870 letters)

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF
1,321,324 sequences; 423,161,544 total letters

Sequences producing significant alignments:	Score (bits)	E Value
gi 24233556 ref NP_705758.1 RIKEN cDNA 4930429A22; hypothe...	1640	0.0
gi 26327097 dbj BAC27292.1 unnamed protein product [Mus mu...]	1605	0.0
gi 25047588 ref XP_129937.2 hypothetical protein MGC37640 ...	1453	0.0
gi 25019857 ref XP_110318.2 similar to hypothetical protei...	1303	0.0
gi 26325590 dbj BAC26549.1 unnamed protein product [Mus mu...]	1166	0.0
gi 23271317 gb AAH36113.1 Unknown (protein for MGC:33943) ...	916	0.0
gi 21753324 dbj BAC04324.1 unnamed protein product [Homo s...]	812	0.0
gi 21292324 gb EAA04469.1 agCP3212 [Anopheles gambiae str....	424	e-117
gi 19115422 ref NP_594510.1 ribonuclease II RNB family pro...	418	e-115
gi 15220899 ref NP_177891.1 putative 3'-5' exoribonuclease...	414	e-114

gi 25406521	pir E96806	hypothetical protein T32E8.1 [imported from UniProtKB]	402	e-110
gi 25332397	pir A84553	probable mitotic control protein di...	396	e-109
gi 24654592	ref NP_728490.1	CG16940-PC [Drosophila melanogaster]	367	e-100
gi 19922976	ref NP_612012.1	CG16940-PA [Drosophila melanogaster]	367	e-100
gi 15292611	gb AAK93574.1	SD10981p [Drosophila melanogaster]	351	2e-95
gi 18488261	ref XP_081229.1	Dis3 [Drosophila melanogaster] ...	350	6e-95
gi 21748526	dbj BAC03400.1	FLJ00327 protein [Homo sapiens]	343	9e-93
gi 26327903	dbj BAC27692.1	unnamed protein product [Mus musculus]	340	7e-92
gi 13446610	emb CAC35051.1	putative exoribonuclease DIS3 [...]	335	2e-90
gi 5262619	emb CAB45749.1	hypothetical protein [Homo sapiens]	334	4e-90
gi 27703387	ref XP_224449.1	similar to mitotic control protein	330	7e-89
gi 19923416	ref NP_055768.2	mitotic control protein dis3 homolog	330	7e-89
gi 6324552	ref NP_014621.1	Possible component of RCC1-Ran GTPase-activating complex	321	3e-86
gi 21297331	gb EAA09476.1	ebiP3704 [Anopheles gambiae strain 2L]	313	6e-84
gi 14250908	emb CAC39259.1	Rrp44p homologue [Trypanosoma brucei]	313	1e-83
gi 19113445	ref NP_596653.1	mitotic control protein dis3 homolog	301	4e-80
gi 15021874	dbj BAB62212.1	hypothetical protein [Macaca fasciata]	291	3e-77
gi 19115966	ref NP_588616.1	hypothetical protein MGC4562 [Homo sapiens]	284	4e-75
gi 18916779	dbj BAB85541.1	KIAA1955 protein [Homo sapiens]	284	5e-75
gi 27369724	ref NP_766107.1	hypothetical protein 4932411M1...	283	9e-75
gi 14250916	emb CAC39263.1	putative ribonuclease II-like protein	278	4e-73
gi 15559519	gb AAH14124.1	AAH14124 Unknown (protein for IMA)	270	1e-70
gi 23136616	gb ZP_00118334.1	hypothetical protein [Cytophaga hylomys]	265	3e-69
gi 19173030	ref NP_597581.1	similarity to DIS3 PROTEIN (RNA binding protein)	260	6e-68
gi 7493807	pir T30524	protein phosphatase Ssd1 homolog - yeast	246	1e-63
gi 22748821	ref NP_689596.1	hypothetical protein MGC42174 [Homo sapiens]	242	2e-62
gi 27685983	ref XP_237349.1	similar to hypothetical protein	241	5e-62
gi 6320499	ref NP_010579.1	Product of gene unknown; Ssd1p [Homo sapiens]	221	3e-56
gi 15616115	ref NP_244420.1	ribonuclease R; virulence-associated protein	214	5e-54
gi 23099883	ref NP_693349.1	ribonuclease R [Oceanobacillus iheyamai]	209	1e-52
gi 21673344	ref NP_661409.1	ribonuclease II family protein	208	4e-52
gi 15672924	ref NP_267098.1	ribonuclease [Lactococcus lactis subsp. lactis]	206	9e-52
gi 21754656	dbj BAC04542.1	unnamed protein product [Homo sapiens]	205	3e-51
gi 23020108	gb ZP_00059814.1	hypothetical protein [Clostridium perfringens]	203	1e-50
gi 16801605	ref NP_471873.1	similar to exoribonuclease RNase P subunit	201	3e-50
gi 16804487	ref NP_465972.1	similar to exoribonuclease RNase P subunit	200	7e-50
gi 21397569	ref NP_653554.1	RNB, RNB-like protein [Bacillus subtilis]	197	7e-49
gi 16080414	ref NP_391241.1	similar to hypothetical protein	195	3e-48
gi 15894003	ref NP_347352.1	FUSION ribonuclease and ribosomal protein	190	7e-47
gi 27467483	ref NP_764120.1	ribonuclease R [Staphylococcus aureus]	190	8e-47
gi 24379988	ref NP_721943.1	putative exoribonuclease R (RNase P subunit)	190	1e-46
gi 19113103	ref NP_596311.1	hypothetical protein; ribonuclease R	188	3e-46
gi 21282471	ref NP_645559.1	ribonuclease R [Staphylococcus aureus]	187	7e-46
gi 15923770	ref NP_371304.1	conserved hypothetical protein	186	1e-45
gi 27685919	ref XP_217466.1	similar to hypothetical protein	186	2e-45
gi 6473411	dbj BAA87129.1	Hypothetical protein [Schizosaccharomyces pombe]	186	2e-45
gi 15926457	ref NP_373990.1	ribonuclease R [Staphylococcus aureus]	185	3e-45
gi 19745621	ref NP_606757.1	putative exoribonuclease R [Streptococcus agalactiae]	185	3e-45
gi 15674608	ref NP_268782.1	putative exoribonuclease R [Streptococcus agalactiae]	184	6e-45
gi 21909888	ref NP_664156.1	putative exoribonuclease R [Streptococcus agalactiae]	183	9e-45
gi 25011590	ref NP_735985.1	Unknown [Streptococcus agalactiae]	183	1e-44
gi 27685993	ref XP_237351.1	similar to hypothetical protein	183	1e-44
gi 22537625	ref NP_688476.1	exoribonuclease, VacB/Rnb family	183	1e-44
gi 15902922	ref NP_358472.1	Exoribonuclease R [Streptococcus agalactiae]	182	2e-44
gi 15900852	ref NP_345456.1	exoribonuclease, VacB/Rnb family	181	3e-44
gi 15673187	ref NP_267361.1	ribonuclease [Lactococcus lactis subsp. lactis]	179	1e-43
gi 15805382	ref NP_294076.1	ribonuclease [Deinococcus radiodurans]	176	2e-42
gi 15605122	ref NP_219907.1	Ribonuclease Family [Chlamydialike organisms]	172	3e-41
gi 15618415	ref NP_224700.1	ribonuclease family [Chlamydophila pneumoniae]	170	1e-40
gi 20807463	ref NP_622634.1	Exoribonucleases [Thermoanaerobacter	169	2e-40
gi 23024105	gb ZP_00063328.1	hypothetical protein [Leuconostoc mesenteroides]	169	2e-40
gi 27380223	ref NP_771752.1	exoribonuclease [Bradyrhizobiaceae]	167	6e-40
gi 15835291	ref NP_297050.1	exoribonuclease, VacB/Rnb family	167	9e-40
gi 23053471	gb ZP_00079680.1	hypothetical protein [Geobacter	166	2e-39
gi 20881074	ref XP_127907.1	RIKEN cDNA 2810028N01 [Mus musculus]	163	1e-38

gi 20071792	gb AAH27357.1	Similar to mitotic control prote...	163	1e-38
gi 15643485	ref NP_228531.1	vacB protein [Thermotoga marit...	162	2e-38
gi 23467938	gb ZP_00123514.1	hypothetical protein [Haemoph...	161	4e-38
gi 15607021	ref NP_214403.1	VacB protein (ribonuclease II ...	160	7e-38
gi 19703943	ref NP_603505.1	Exoribonuclease II [Fusobacter...	160	8e-38
gi 18310278	ref NP_562212.1	ribonuclease R [Clostridium pe...	160	1e-37
gi 23038196	gb ZP_00070371.1	hypothetical protein [Oenococ...	159	1e-37
gi 15642594	ref NP_232227.1	ribonuclease R [Vibrio cholera...	159	2e-37
gi 17545947	ref NP_519349.1	PROBABLE EXORIBONUCLEASE RNASE...	158	5e-37
gi 22995402	gb ZP_00039879.1	hypothetical protein [Xylella...	157	8e-37
gi 16763187	ref NP_458804.1	ribonuclease R (RNase R) [Salm...	157	8e-37
gi 22954374	gb ZP_00002175.1	hypothetical protein [Nitroso...	156	1e-36
gi 16132001	ref NP_418600.1	putative enzyme [Escherichia c...	156	1e-36
gi 15804768	ref NP_290809.1	putative enzyme [Escherichia c...	156	1e-36
gi 731093	sp P21499 RNR_ECOLI	Ribonuclease R (RNase R) (Vac...	156	1e-36
gi 391901	dbj BAA01777.1	ORF-2 [Shigella flexneri]	155	2e-36
gi 24115534	ref NP_710044.1	putative enzyme [Shigella flex...	155	2e-36
gi 27735249	sp P30851 RNR_SHIFL	Ribonuclease R (RNase R) (V...	155	2e-36
gi 26553786	ref NP_757720.1	3'-5' exoribonuclease RNase R ...	155	2e-36
gi 27364704	ref NP_760232.1	Exoribonuclease R [Vibrio vuln...	154	5e-36
gi 21242317	ref NP_641899.1	RNase R [Xanthomonas axonopodi...	154	5e-36
gi 15600130	ref NP_253624.1	exoribonuclease RNase R [Pseud...	154	5e-36
gi 23003758	gb ZP_00047408.1	hypothetical protein [Lactoba...	154	6e-36
gi 26251071	ref NP_757111.1	Ribonuclease R [Escherichia co...	154	6e-36
gi 11359056	pir T45283	growth polarity maintenance protein...	154	7e-36

Alignments

>gi|24233556|ref|NP_705758.1| RIKEN cDNA 4930429A22; hypothetical protein
MGC37640 [Mus musculus]
gi|23273603|gb|AAH36177.1| Unknown (protein for MGC:37640) [Mus musculus]
Length = 870

Score = 1640 bits (4247), Expect = 0.0
Identities = 818/870 (94%), Positives = 818/870 (94%)

Query: 1	MNHPDYKLNLRXXXXXXXXXXXXXXXXXXXXXXIFETYMSKEDVS	60
	MNHPDYKLNLR	D
Sbjct: 1	MNHPDYKLNLRSPGTPRGVSSVGPSAVGASPDKSKNKSMRGKKSI	FETYMSKEDVS
	60	
Query: 61	EGLKRGTLIQGVLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNGDLVVVKLLPEDQ	120
	EGLKRGTLIQGVLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNGDLVVVKLLPEDQ	
Sbjct: 61	EGLKRGTLIQGVLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNGDLVVVKLLPEDQ	120
Query: 121	WKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSGPDI	180
	IEAQFDDSDSEDRHGN	
Sbjct: 121	WKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSGPDI	180
	IEAQFDDSDSEDRHGN	
Query: 181	TSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPQDTRGLSEKSLQKSAKVYILEKK	240
	TSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPQDTRGLSEKSLQKSAKVYILEKK	
Sbjct: 181	TSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPQDTRGLSEKSLQKSAKVYILEKK	240
Query: 241	HSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFMTRPKDFANTLF	300
	HSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFMTRPKDFANTLF	
Sbjct: 241	HSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFMTRPKDFANTLF	300
Query: 301	CRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGDFSDSSEVLECLPQSLPWT	360
	CRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGDFSDSSEVLECLPQSLPWT	
Sbjct: 301	CRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGDFSDSSEVLECLPQSLPWT	360
Query: 361	IPPDEVGKRRDLRKDCIFTIDPSTARLDALACRRLTDGTFEVGVHIADVSYFPEGSS	420
	IPPDEVGKRRDLRKDCIFTIDPSTARLDALACRRLTDGTFEVGVHIADVSYFPEGSS	
Sbjct: 361	IPPDEVGKRRDLRKDCIFTIDPSTARLDALACRRLTDGTFEVGVHIADVSYFPEGSS	420
Query: 421	LDKVAERATSVYLVQKVVPMPLPRLCEELCSLNPMTDKLTFSVIWKLTPEGKILEEWFG	480

LDKVAEAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPEGKILEEWFG
Sbjct: 421 LDKVAEAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPEGKILEEWFG 480

Query: 481 RTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXXXHSVEEVHQAVLNLSIAKQLRRQ 540
RTIIRSCTKLSYDHAQSMIEN HSVEEVHQAVLNLSIAKQLRRQ
Sbjct: 481 RTIIRSCTKLSYDHAQSMIENPTEKIPPEEELPPISPEHSVEEVHQAVLNLSIAKQLRRQ 540

Query: 541 RFVDGALRDLQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFP 600
RFVDGALRDLQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFP
Sbjct: 541 RFVDGALRDLQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFP 600

Query: 601 EQALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKS LT KTFGDDKYSLARKEVLT 660
EQALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKS LT KTFGDDKYSLARKEVLT
Sbjct: 601 EQALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKS LT KTFGDDKYSLARKEVLT 660

Query: 661 NMYSRPMQM ALYFCSGMLQDQE QFRHYALNVPLYTHFTSPIRRFADIVVHRL LAAALGYS 720
NMYSRPMQM ALYFCSGMLQDQE QFRHYALNVPLYTHFTSPIRRFADIVVHRL LAAALGYS
Sbjct: 661 NMYSRPMQM ALYFCSGMLQDQE QFRHYALNVPLYTHFTSPIRRFADIVVHRL LAAALGYS 720

Query: 721 EQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVLVKGESGPLESEAMVMGVLNQAF 780
EQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVLVKGESGPLESEAMVMGVLNQAF
Sbjct: 721 EQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVLVKGESGPLESEAMVMGVLNQAF 780

Query: 781 DVLVLRFGVQKRIYCNALALRSYSFQKVGGKPELTLWEPDDLEEEPTQQVITIFSLVDV 840
DVLVLRFGVQKRIYCNALALRSYSFQKVGGKPELTLWEPDDLEEEPTQQVITIFSLVDV
Sbjct: 781 DVLVLRFGVQKRIYCNALALRSYSFQKVGGKPELTLWEPDDLEEEPTQQVITIFSLVDV 840

Query: 841 VLQAEATALKYSAILKRPGLEKASDEEPED 870
VLQAEATALKYSAILKRPGLEKASDEEPED
Sbjct: 841 VLQAEATALKYSAILKRPGLEKASDEEPED 870

>gi|26327097|dbj|BAC27292.1| unnamed protein product [Mus musculus]
Length = 831

Score = 1605 bits (4155), Expect = 0.0
Identities = 801/831 (96%), Positives = 801/831 (96%), Gaps = 14/831 (1%)

Query: 54 MSKEDVSEGLKRGT LIQGVLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNGDLVVV 113
MSKEDVSEGLKRGT LIQGVLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNGDLVVV
Sbjct: 1 MSKEDVSEGLKRGT LIQGVLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNGDLVVV 60

Query: 114 KLLPEDQWK-----AVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWS 159
KLLPEDQWK AVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWS
Sbjct: 61 KLLPEDQWKPRITSLPGVLGLQAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWS 120

Query: 160 GPDVIIEAQFDDSDSED RHGNTSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPQDT 219
GPDVIIEAQFDDSDSED RHGNTSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPQDT
Sbjct: 121 GPDVIIEAQFDDSDSED RHGNTSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPQDT 180

Query: 220 RGLSEKSLQSAKVVYILEKKHSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVP 279
RGLSEKSLQSAKVVYILEKKHSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVP
Sbjct: 181 RGLSEKSLQSAKVVYILEKKHSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVP 240

Query: 280 LKDCPQDFMTRPKDFANTLFICRIIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYG 339
LKDCPQDFMTRPKDFANTLFICRIIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYG
Sbjct: 241 LKDCPQDFMTRPKDFANTLFICRIIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYG 300

Query: 340 VDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARLDLACRRLTD 399
VDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARLDLACRRLTD
Sbjct: 301 VDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARLDLACRRLTD 360

Query: 400 GTFEVGVHIADVSYFVPEGSSLKVAEAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDK 459
GTFEVGVHIADVSYFVPEGSSLKVAEAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDK
Sbjct: 361 GTFEVGVHIADVSYFVPEGSSLKVAEAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDK 420

Query: 460 LTFSVIWKLTPKGKILEEWFGRTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXHS 519
LTFSVIWKLTPKGKILEEWFGRTIIRSCTKLSYDHAQSMIEN HS
Sbjct: 421 LTFSVIWKLTPKGKILEEWFGRTIIRSCTKLSYDHAQSMIENPTEKIPPEELPPISPEHS 480

Query: 520 VEEVHQAVLNLSIAKQLRRQRFDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKL 579
VEEVHQAVLNLSIAKQLRRQRFDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKL
Sbjct: 481 VEEVHQAVLNLSIAKQLRRQRFDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKL 540

Query: 580 VEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCQDMGLPMDVSSAGALN 639
VEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCQDMGLPMDVSSAGALN
Sbjct: 541 VEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCQDMGLPMDVSSAGALN 600

Query: 640 KSLTKTFGDDKYSLARKEVLTNMYSRPMQMALYFCGMLQDQEQRHYALNVPLYTHFTS 699
KSLTKTFGDDKYSLARKEVLTNMYSRPMQMALYFCGMLQDQEQRHYALNVPLYTHFTS
Sbjct: 601 KSLTKTFGDDKYSLARKEVLTNMYSRPMQMALYFCGMLQDQEQRHYALNVPLYTHFTS 660

Query: 700 PIRRFADVIVHRLAALGYSEQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVL 759
PIRRFADVIVHRLAALGYSEQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVL
Sbjct: 661 PIRRFADVIVHRLAALGYSEQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVL 720

Query: 760 VKESGPLESEAMVMGVLNQAFDVLVLRFGVQKRIYCNALALRSYSFQKVGGKPELTLVWE 819
VKESGPLESEAMVMGVLNQAFDVLVLRFGVQKRIYCNALALRSYSFQKVGGKPELTLVWE
Sbjct: 721 VKESGPLESEAMVMGVLNQAFDVLVLRFGVQKRIYCNALALRSYSFQKVGGKPELTLVWE 780

Query: 820 PDDLEEEPTQQVITIFSLVDVVLQAEATALKYSAILKRPGLEKASDEEPED 870
PDDLEEEPTQQVITIFSLVDVVLQAEATALKYSAILKRPGLEKASDEEPED
Sbjct: 781 PDDLEEEPTQQVITIFSLVDVVLQAEATALKYSAILKRPGLEKASDEEPED 831

>gi|25047588|ref|XP_129937.2| hypothetical protein MGC37640 [Mus musculus]
Length = 819

Score = 1453 bits (3762), Expect = 0.0
Identities = 720/772 (93%), Positives = 720/772 (93%)

Query: 1 MNHPDYKLNLRXXXXXXXXXXXXXXXXXXXXXXXXXXXXIFETYMSKEDVS 60
MNHPDYKLNLR D IFETYMSKEDVS
Sbjct: 1 MNHPDYKLNLRSPGTPRGVSSVVGPSAVGASPGDKSKNKS MRGKKSI FETYMSKEDVS 60

Query: 61 EGLKRGTLIQGVLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNGDLVVVKLLPEDQ 120
EGLKRGTLIQGVLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNGDLVVVKLLPEDQ
Sbjct: 61 EGLKRGTLIQGVLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNGDLVVVKLLPEDQ 120

Query: 121 WKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSGPDVIIEAQFDDSDSEDRHGN 180
WKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSGPDVIIEAQFDDSDSEDRHGN
Sbjct: 121 WKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSGPDVIIEAQFDDSDSEDRHGN 180

Query: 181 TSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPIPQDTRGLSEKSLQSAKVVYILEKK 240
TSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPIPQDTRGLSEKSLQSAKVVYILEKK
Sbjct: 181 TSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPIPQDTRGLSEKSLQSAKVVYILEKK 240

Query: 241 HSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFMTRPKDFANTLF 300
HSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFMTRPKDFANTLF
Sbjct: 241 HSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFMTRPKDFANTLF 300

Query: 301 CRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDSSEVLECLPQSLPWT 360
CRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDSSEVLECLPQSLPWT
Sbjct: 301 CRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDSSEVLECLPQSLPWT 360

Query: 361 IPPDEVGKRRDLRKDCIFTIDPSTARLDALACRRLTDGTFEVGVHIADVSYFPEGSS 420
IPPDEVGKRRDLRKDCIFTIDPSTARLDALACRRLTDGTFEVGVHIADVSYFPEGSS
Sbjct: 361 IPPDEVGKRRDLRKDCIFTIDPSTARLDALACRRLTDGTFEVGVHIADVSYFPEGSS 420

Query: 421 LDKVAAERATSVYLVQKVVPMPLPRLCEELCSLNPMTDKLTFSVIWKLTPKGKILEEWF 480
LDKVAAERATSVYLVQKVVPMPLPRLCEELCSLNPMTDKLTFSVIWKLTPKGKILEEWF
Sbjct: 421 LDKVAAERATSVYLVQKVVPMPLPRLCEELCSLNPMTDKLTFSVIWKLTPKGKILEEWF 480

Query: 481 RTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXHSVEEVHQAVLNLSIAKQLRRQ 540
RTIIRSCTKLSYDHAQSMIEN HSVEEVHQAVLNLSIAKQLRRQ
Sbjct: 481 RTIIRSCTKLSYDHAQSMIENPTEKIPEEEELPPISPEHSVEEVHQAVLNLSIAKQLRRQ 540

Query: 541 RFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFP 600
RFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFP
Sbjct: 541 RFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFP 600

Query: 601 EQALLRRHPPPQTKMLSDLVEFCDQMGLPMMDVSSAGALNKS LT KTFGDDKYSLARKEVLT 660
EQALLRRHPPPQTKMLSDLVEFCDQMGLPMMDVSSAGALNKS LT KTFGDDKYSLARKEVLT
Sbjct: 601 EQALLRRHPPPQTKMLSDLVEFCDQMGLPMMDVSSAGALNKS LT KTFGDDKYSLARKEVLT 660

Query: 661 NMYSRPMQM ALYFCSGMLQDQE QFRHY ALNVPL YTHFTSPIR FAD VIVH RLLA AALGYS 720
NMYSRPMQM ALYFCSGMLQDQE QFRHY ALNVPL YTHFTSPIR FAD VIVH RLLA AALGYS
Sbjct: 661 NMYSRPMQM ALYFCSGMLQDQE QFRHY ALNVPL YTHFTSPIR FAD VIVH RLLA AALGYS 720

Query: 721 EQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVLVKE SGPLESEAMV 772
EQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVLVKE SGPLESEAMV
Sbjct: 721 EQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVLVKE SGPLESEAMV 772

>gi|25019857|ref|XP_110318.2| similar to hypothetical protein MGC37640 [Mus musculus]
Length = 663

Score = 1303 bits (3371), Expect = 0.0
Identities = 647/663 (97%), Positives = 647/663 (97%)

Query: 208 MKDENTPI PQDTRGLSEKSLQKSAKVVYILEKKHSRAATGILKLLADKNSDLFKKYALFS 267
MKDENTPI PQDTRGLSEKSLQKSAKVVYILEKKHSRAATGILKLLADKNSDLFKKYALFS
Sbjct: 1 MKDENTPI PQDTRGLSEKSLQKSAKVVYILEKKHSRAATGILKLLADKNSDLFKKYALFS 60

Query: 268 PSDHRVPRIYVPLKDCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEI 327
PSDHRVPRIYVPLKDCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEI
Sbjct: 61 PSDHRVPRIYVPLKDCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEI 120

Query: 328 EPETEGILTEYGVDFSDSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARD 387
EPETEGILTEYGVDFSDSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARD
Sbjct: 121 EPETEGILTEYGVDFSDSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARD 180

Query: 388 LDDALACRRLTDGTFEVGVIADVSYFVPEGSSLDKVAERATSVYLVQKVVPMLPRLLC 447
LDDALACRRLTDGTFEVGVIADVSYFVPEGSSLDKVAERATSVYLVQKVVPMLPRLLC
Sbjct: 181 LDDALACRRLTDGTFEVGVIADVSYFVPEGSSLDKVAERATSVYLVQKVVPMLPRLLC 240

Query: 448 EELCSLNPM TDKLTFSVIWKLTP EGKILEEWFGRTI IIRSCTKLSYDHAQSMIENXXXXX 507
EELCSLNPM TDKLTFSVIWKLTP EGKILEEWFGRTI IIRSCTKLSYDHAQSMIEN
Sbjct: 241 EELCSLNPM TDKLTFSVIWKLTP EGKILEEWFGRTI IIRSCTKLSYDHAQSMIENPTEKIP 300

Query: 508 XXXXXXXXXXXXHSVEEVHQAVLNLSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQG 567
HSVEEVHQAVLNLSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQG
Sbjct: 301 EEELPPISPEHSVEEVHQAVLNLSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQG 360

Query: 568 CHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCDQMG 627
CHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCDQMG
Sbjct: 361 CHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCDQMG 420

Query: 628 LPMDVSSAGALNKS LT KTFGDDKYSLARKEVLT NMYSPRMQM ALYFCSGMLQDQE QFRHY 687
LPMDVSSAGALNKS LT KTFGDDKYSLARKEVLT NMYSPRMQM ALYFCSGMLQDQE QFRHY
Sbjct: 421 LPMDVSSAGALNKS LT KTFGDDKYSLARKEVLT NMYSPRMQM ALYFCSGMLQDQE QFRHY 480

Query: 688 ALNVPLYTHFTSPIR FAD VIVH RLLA AALGYS EQPDVEPDTLQKQADHCNDRRMASKRV 747
ALNVPLYTHFTSPIR FAD VIVH RLLA AALGYS EQPDVEPDTLQKQADHCNDRRMASKRV
Sbjct: 481 ALNVPLYTHFTSPIR FAD VIVH RLLA AALGYS EQPDVEPDTLQKQADHCNDRRMASKRV 540

Query: 748 QELSIGLFFAVLVKE SGPLESEAMVMGVLNQAFDVLVLRFGVQKR IYCNALALRSYSFQK 807

QELSIGLFFAVLVKESGPLESEAMVMGVLNQAFDVLVLRFGVQKRIYCNALALRSYSFQK
Sbjct: 541 QELSIGLFFAVLVKESGPLESEAMVMGVLNQAFDVLVLRFGVQKRIYCNALALRSYSFQK 600

Query: 808 VGKKPELTWEPDDLEEEPTQQVITIFSLVDVVLQAEATALKYSAILKRPGLEKASDEE 867
VGKKPELTWEPDDLEEEPTQQVITIFSLVDVVLQAEATALKYSAILKRPGLEKASDEE
Sbjct: 601 VGKKPELTWEPDDLEEEPTQQVITIFSLVDVVLQAEATALKYSAILKRPGLEKASDEE 660

Query: 868 PED 870
PED
Sbjct: 661 PED 663

>gi|26325590|dbj|BAC26549.1| unnamed protein product [Mus musculus]
Length = 684

Score = 1166 bits (3016), Expect = 0.0
Identities = 569/590 (96%), Positives = 570/590 (96%)

Query: 150 PLQQSRKGWSPDVIIEAQFDDSDSEDRHGNTSGLVDGVKKLSISTPDRGKEDSSTPVMK 209
P +RKGWSPDVIIEAQFDDSDSEDRHGNTSGLVDGVKKLSISTPDRGKEDSSTPVMK
Sbjct: 14 PCSSARKGWSPDVIIEAQFDDSDSEDRHGNTSGLVDGVKKLSISTPDRGKEDSSTPVMK 73

Query: 210 DENTPIPQDTRGLSEKSLQSAKVVYILEKKHSRAATGILKLLADKNSDLFKKYALFSPS 269
DENTPIPQDTRGLSEKSLQSAKVVYILEKKHSRAATGILKLLADKNSDLFKKYALFSPS
Sbjct: 74 DENTPIPQDTRGLSEKSLQSAKVVYILEKKHSRAATGILKLLADKNSDLFKKYALFSPS 133

Query: 270 DHRVPRIYVPLKDCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEIEP 329
DHRVPRIYVPLKDCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEIEP
Sbjct: 134 DHRVPRIYVPLKDCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEIEP 193

Query: 330 ETEGILTEYGVDFSDSSEVLECLPQLPWTIPPDEVGKRRDLRKDCIFTIDPSTARLD 389
ETEGILTEYGVDFSDSSEVLECLPQLPWTIPPDEVGKRRDLRKDCIFTIDPSTARLD
Sbjct: 194 ETEGILTEYGVDFSDSSEVLECLPQLPWTIPPDEVGKRRDLRKDCIFTIDPSTARLD 253

Query: 390 DALACRRLTDGTFEVGVHIADVSYFPEGSSLKDVAERATSVYLVQKVPMLPRLLCEE 449
DALACRRLTDGTFEVGVHIADVSYFPEGSSLKDVAERATSVYLVQKVPMLPRLLCEE
Sbjct: 254 DALACRRLTDGTFEVGVHIADVSYFPEGSSLKDVAERATSVYLVQKVPMLPRLLCEE 313

Query: 450 LCSLPMTDKLTFSVIWKLTPEGKILEEWFGRTIIRSCTKLSYDHAQSMIENXXXXXXXXX 509
LCSLPMTDKLTFSVIWKLTPEGKILEEWFGRTIIRSCTKLSYDHAQSMIEN
Sbjct: 314 LCSLPMTDKLTFSVIWKLTPEGKILEEWFGRTIIRSCTKLSYDHAQSMIENPTEKIP 373

Query: 510 XXXXXXXXHSVEEVHQAVLNLSIAKQLRRQRFDGALRLDQLKLAFTLDHETGLPQGCH 569
HSVEEVHQAVLNLSIAKQLRRQRFDGALRLDQLKLAFTLDHETGLPQGCH
Sbjct: 374 ELPPISPEHSVEEVHQAVLNLSIAKQLRRQRFDGALRLDQLKLAFTLDHETGLPQGCH 433

Query: 570 IYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCQMDGP 629
IYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCQMDGP
Sbjct: 434 IYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCQMDGP 493

Query: 630 MDVSSAGALNKSLTTFGDDKYSLARKEVLTNMYSRPMQMALYFCGMLQDQEQRHYAL 689
MDVSSAGALNKSLTTFGDDKYSLARKEVLTNMYSRPMQMALYFCGMLQDQEQRHYAL
Sbjct: 494 MDVSSAGALNKSLTTFGDDKYSLARKEVLTNMYSRPMQMALYFCGMLQDQEQRHYAL 553

Query: 690 NVPLYTHFTSPIRFADIVVHRLLAALGYSEQPDVEPDTLQKQADHCND 739
NVPLYTHFTSPIRFADIVVHRLLA LGYSEQPDVEPDTLQKQADHCND
Sbjct: 554 NVPLYTHFTSPIRFADIVVHRLLAAGLGYSEQPDVEPDTLQKQADHCND 603

>gi|23271317|gb|AAH36113.1| Unknown (protein for MGC:33943) [Homo sapiens]
Length = 612

Score = 916 bits (2368), Expect = 0.0
Identities = 451/532 (84%), Positives = 476/532 (89%), Gaps = 2/532 (0%)

Query: 49 IFETYMSKEDVSEGLKRGTLIQGVLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNG 108
IFETYMSKEDVSEGLKRGTLIQGVLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNG

Sbjct: 42 IFETYMSKEDVSEGLKRGTЛИQGVLRINPKFHEAFIPSPDGDRDIFIDGVVARNRALNG 101

Query: 109 DLVVVKLLPEDQWKAVKPESNDKEIEATYEADIEEGCGHHPLQQSRKGWS-GPDVIIEA 167
DLVVVKLLPE+ WK VKPESNDKE EA YE+DIPEE CGHH QQS K ++ PDVI+EA

Sbjct: 102 DLVVVKLLPEEHWKVVKPESNDKETEAAYESDIPEELCGHHLQQSLKSYNDSPDVIVEA 161

Query: 168 QFDDSDSEDRHGNTSG-LVDGVKKLSISTPDRGKEDSSTPVMKDENTPI PQDTRGLSEKS 226
QFD SDSED HG T LVDGVKKLS+ ++G+ED PV KDE T I QDTR LSEKS

Sbjct: 162 QFDGSDSEDGHGITQNVLVDGVKKLSVCSEKGREDGDAPVTKDETTCISQDTRALSEKS 221

Query: 227 LQSAKVVYILEKKHSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQD 286
LQ+SAKVVYILEKKHSRAATG LKLLADKNS+LF+KYALFSPSDHRVPRIYVPLKDCPQD

Sbjct: 222 LQRSAKVVYILEKKHSRAATGFLKLLADKNSELFRKYALFSPSDHRVPRIYVPLKDCPQD 281

Query: 287 FMTRPKDFANTLFICRI IDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFS 346
F+ RPKD+ANTLFICRI +DWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFS

Sbjct: 282 FVARPKDYANTLFICRIVDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFS 341

Query: 347 SEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARLDLACRRLTDGTFEVGV 406
SEVLECLPQ LPWTIPP+E KRRDLRKDCIFTIDPSTARLDLDDAL+C+ L DG F+VGV

Sbjct: 342 SEVLECLPQGLPWTIPPEFSKRRDLRKDCIFTIDPSTARLDLDDALSCKPLADGNFKVGV 401

Query: 407 HIADVSYFVPEGSSLDKVAERATSVYLVQKVVPMPLRLLCEELCSLNPMTDKLTFSVIW 466
HIADVSYFVPEGS LDKVAERATSVYLVQKVVPMPLRLLCEELCSLNPM+DKLTFSVIW

Sbjct: 402 HIADVSYFVPEGSDLDKVAERATSVYLVQKVVPMPLRLLCEELCSLNPMSDKLTFSVIW 461

Query: 467 KLTPEGKILEEWFGRTIIRSKTLYDHAQSMIENXXXXXXXXXXXXHSVEEVHQ 526
LTPEGKIL+EWFGRTIIRSKTLY+HAQSMIE+ HS EEVHQ

Sbjct: 462 TLTPEGKILDEWFGRITIIRSKTLYEHAQSMIESPTEKIPAKELPPISPEHSSEEVHQ 521

Query: 527 VNLHSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNK 578
VNLH IAKQLR+QRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYR+SNK

Sbjct: 522 VNLHGIAKQLRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRESNK 573

>gi|21753324|dbj|BAC04324.1| unnamed protein product [Homo sapiens]
Length = 603

Score = 812 bits (2098), Expect = 0.0
Identities = 410/527 (77%), Positives = 436/527 (82%), Gaps = 2/527 (0%)

Query: 1 MNHPDYKLNRLXXXXXXXXXXXXXXXXXXXXXXXXXIFETYMSKEDVS 60
M+HPDY++NLR D IFETYMSKEDVS

Sbjct: 1 MSHPDYRMNLRPLGTPRGVSAVAGPHDIGASPGDKSKNRSTRGKKKSIFETYMSKEDVS 60

Query: 61 EGLKRGTЛИQGVLRINPKFHEAFIPSPDGDRDIFIDGVVARNRALNGDLVVVKLLPEDQ 120
EGLKRGTЛИQGVLRINPKFHEAFIPSPDGDRDIFIDGVVARNRALNGDLVVVKLLPE+

Sbjct: 61 EGLKRGTЛИQGVLRINPKFHEAFIPSPDGDRDIFIDGVVARNRALNGDLVVVKLLPEEH 120

Query: 121 WKAVKPESNDKEIEATYEADIEEGCGHHPLQQSRKGWS-GPDVIIEAQFDDSDEDRHG 179
WK VKPESNDKE EA YE+DIPEE CGHH QQS K ++ PDVI+EAQFD SDSED HG

Sbjct: 121 WKVVKPESNDKETEAAYESDIPEELCGHHLQQSLKSYNDSPDVIVEAQFDGSDSEDGHG 180

Query: 180 NTSG-LVDGVKKLSISTPDRGKEDSSTPVMKDENTPI PQDTRGLSEKSLQSAKVVYILE 238
T LVDGVKKLS+ ++G+ED PV KDE T I QDTR LSEKSLQ+SAKVVYILE

Sbjct: 181 ITQNVLVDGVKKLSVCSEKGREDGDAPVTKDETTCISQDTRALSEKSLQRSAKVVYILE 240

Query: 239 KKHSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFMTRPKDFANTL 298
KKHSRAATG LKLLADKNS+LF+KYALFSPSDHRVPRIYVPLKDCPQDF+ RPKD+ANTL

Sbjct: 241 KKHSRAATGFLKLLADKNSELFRKYALFSPSDHRVPRIYVPLKDCPQDFVARPKDYANTL 300

Query: 299 FICRI IDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLP 358
FICRI+DWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQ LP

Sbjct: 301 FICRIVDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQGLP 360

Query: 359 WTIPPDEVGKRRDLRKDCIFTIDPSTARLDLACRRLTDGTFEVGVHIADVSYFPEG 418

WTIPP+E KRRDLRKDCIFTIDPSTARLDLDDAL+C+ L DG F+VGVHIADVSYFVPEG
Sbjct: 361 WTIPPEFSKRRDLRKDCIFTIDPSTARLDLDDALSCKPLADGNFKVGVHIADVSYFVPEG 420

Query: 419 SS LD KVAAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPEGKILEEW 478
S LDKVAAERATSVYLVQKVVPMLPRLLCEELCSLNPM+DKLTFSVIWKLTPEGKIL+EW
Sbjct: 421 SD LD KVAAERATSVYLVQKVVPMLPRLLCEELCSLNPMSDKLTFSVIWKLTPEGKILDEW 480

Query: 479 FGRTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXHSVEEVHQ 525
FGRTIIRSCTKLSY+HAQSMIE+ HS EEVHQ
Sbjct: 481 FGRTIIRSCTKLSYEHAQSMIESPTEKIPAKELPPISPEHSSEEVHQ 527

>gi|21292324|gb|EAA04469.1| agCP3212 [Anopheles gambiae str. PEST]
Length = 794

Score = 424 bits (1089), Expect = e-117
Identities = 249/672 (37%), Positives = 379/672 (56%), Gaps = 35/672 (5%)

Query: 196 PDRGKEDSSTPVMDENTPIQD--TRGLSEKSLQKSAK-VVYILEKKHSRAATGILKLL 252
P +DS+T + N ++ T+ KS Q S VV ILEK+H+R G K L
Sbjct: 127 PKAPSDDSATSPNANGNDESAAEDATQQAGGKSTQNSVGFVVAILEKRHNRQCVG--KFL 184

Query: 253 ADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFM-----TRP 291
A K Y +F P D R+P + V +D P + T
Sbjct: 185 AAPGK--KHYRVFMPRDMRIPPVRVFQDWPNALLSTNIAKLKDDKEEKEDRKVPQTGD 242

Query: 292 KDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDSSEVLE 351
D + L+ II+W++ +G + KS+G+ G +E E E IL E+ +D + + +L
Sbjct: 243 VDVTDVLYQAEIIIEWQDEV--PIGTILKSIGKCGVLEVENESILVEHNLDVTPYGEAILA 300

Query: 352 CLPQSLPWTTIPPDEVGKRRDLRKDCIFTIDPSTARLDLDDALACRRLTDGTFEVGVHIADV 411
LP ++P+ IP +E+ +R DLR +CIFTIDP+TARDLDDAL+C++L +G ++++GVHI+DV
Sbjct: 301 QLP-AVPYCIPQEELERREDLRGECIFTIDPATARDLDDALSCKQLENGNYQIGVHISDV 359

Query: 412 SYFPEGSSLDKVAAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPE 471
+YF+ E S LD++ RAT+S+Y+V V MLP+ LC CSL P DKL FSV W++ P+
Sbjct: 360 TYFLRESSPLDELVKLRATSIYMVDVTYHMLPKQLCNT-CSLLPGEDKLAFAFWEMQPD 418

Query: 472 GKILEEWFGRTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXHSVEEVHQAVLNH 531
G +L F RT+I SC++LSY+HAQ M++N ++ +++ + V L
Sbjct: 419 GTVLSTRFARTVINSCSQLSYEHAQLMDNPSCEVEEDQFPEIMHGYNAKQLCKIVNTLQ 478

Query: 532 SIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAV 591
SIA QLR++R DG L+++Q KL F LD TG P +Y+ R SN+++E+FMILLAN +V
Sbjct: 479 SIAVQLRQRRMDDGCLKINQPKLTFRLDPATGRPIEYGVYKVRPSNEMIEDFMILLANTS 538

Query: 592 AHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKS LT KTFGDDKY 651
A+ I++ FPE +LLR H PP M+ +LV G + +S + + + +
Sbjct: 539 ANAIYKAFPEISLLRAHSPPAENMMKNLVRTLSSLGHALS YASPKDIRECMETIITTSEN 598

Query: 652 SLARKEVLTNMYSRPMQMALYFCGMLQDQEQRHYALNVPLYTHFTSPIRRAVIVHR 711
A + VL+ + ++PM A Y+CS E F HYAL +P+YTHFTSPIRRAVIVHR
Sbjct: 599 PDATRSVLSVLLAKPMIRAQYYCSLYATTPEHFMHYALAIPMYTHFTSPIRRYADCLVHR 658

Query: 712 LLAAALGYSEQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVLVKESGPLESEAM 771
+LAAAL QP P+ LQ A CN+++ +K E S L+F ++ G E+EA
Sbjct: 659 VLAAAALAI DVQPKRSPEELQCLAMICNEKKYNAKCAGEASSLLYFRHWLEAVGEYETEAA 718

Query: 772 VMGVLNQAFDVLVLRFGVQKRIYCNALALRSYSFQKVGKKPELTLVWEPPDDLEEPTQQV 831
VMG +++++ G+ + L+ + K +P + + P+D P +
Sbjct: 719 VMGYAAHHIELVLIHSGIVLKAATKKLSTVATVVYK-PTEPVASCMLIPNDTSIPPVE-- 775

Query: 832 ITIFSLVDVVLQ 843
+TIF+ V V ++
Sbjct: 776 LTIFTKVRVTVK 787

>gi|19115422|ref|NP_594510.1| ribonuclease II RNB family protein; dis3-like [Schizosaccharomyces pombe]
gi|7493295|pir||T38518 ribonuclease II RNB family protein - fission yeast (Schizosaccharomyces pombe)
gi|2414618|emb|CAB16367.1| ribonuclease II RNB family protein; dis3-like [Schizosaccharomyces pombe]
Length = 927

Score = 418 bits (1075), Expect = e-115
Identities = 273/764 (35%), Positives = 392/764 (51%), Gaps = 91/764 (11%)

Query: 49 IFETYMSKEDVSEGLKRGTЛИQGVLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNG 108
++ Y V +GLK GTL +G LRI H + + D ++DG +ARNRA +
Sbjct: 175 VYPLYYYDSATVKKGLKSGTLFKGTLRILEN--HRSAFACMEDIPDFYVDGPIARNRAFHН 232

Query: 109 DLVVVKLLPEDQWKAVKPESNDKEIEATYEADIPPEEGCGHHPLQQSRKGWSGPDVIIEAQ 168
D+V+V E D P E LQ + + +
Sbjct: 233 DVVIV-----EPVMNNDSPTEKSNF--LQNG-----VEVKV 261

Query: 169 FDDSDSEDRHGNTSGLVKKLSISTPDRGKEDSSTPVMKDENTPIPQDTRGLSEKSLQ 228
D D E G ++ +++L I + K DS T
Sbjct: 262 IKDHDE----LGGAMEHLERLEIKSVASFKGDSRT----- 293

Query: 229 KSAKVYYILEKKHSRAATGILKL--LADKNSDLFKK---YALFSPSDHRVPRIYVPLKDC 283
A+VV I ++ GIL+ + KN + K YA+F P D R+P I + D
Sbjct: 294 -RARVVAIEKRAEISKIVGILRAPGWSLNVEYVSKSSYAIFIPKDKRLPFITIHKNDL 352

Query: 284 P----QDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYG 339
++++ + LF I W + +G L + LG ++E T +L E G
Sbjct: 353 SDLSGENWIENILKHHDQLFSVEITRWSIYSRYPGMGVLGKGNITDVEAYTNALLENG 412

Query: 340 VDFSDFSSEVLECLPQSLPWTTIPDEVGKRRDLRKDCIFTIDPSTARLDALACRRLTD 399
+ S FS EVL CLP W I +E+ KRRDLR + I TIDP TARLDAA++CR L +
Sbjct: 413 ISSSPFSDEVLNCLPPD-DWIISHEEIKKRRDLRNELIITIDPETARDLDAVSCRALDN 471

Query: 400 GTFEVGVHIADVSYFVPEGSSLKDVAEARATSVYLVQKVPMLPRLLCEELCSLNPMTDK 459
GT+EVGVHIADV++FV S+LDK AA RAT+VYLVQK +PMLP LLCE LCSLNP ++
Sbjct: 472 GTYEVGVHIADVTHFKPDSALDKEASRATTVYLVQKAIPMLPPLLcerlcslnpnver 531

Query: 460 LTFSVIWKLTPEGK-ILEEWFGRTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXXX 518
L FSV WKL GK I + WFG+T+I++C +L+Y AQ +IE H
Sbjct: 532 LAFSVFWKLDNSNGKEIGKRWFGKTVIKTCARLAYSEAQGVIEG--KSWDDAVGKPIGGTH 589

Query: 519 SVEEVHQAVLNLSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNK 578
+ ++V ++L L I++LR+ RF GA+ ++ +L F LD E G+P C +YE D+N
Sbjct: 590 TPKDVENTSILTCEISRKLRKDRFAKGAVEINSTELKFQLD-EYGMNKCEVYEQTDANH 648

Query: 579 LVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQTCKMLSDLVEFCDCQMLPMDVSSAGAL 638
L+EEFMLAN +VA I + F +LLRRH P+ K +++ F M D SS+ A
Sbjct: 649 LIEEFMLLANRSVAEHISKNFSNNSSLRRHASPKEKQINEFCHFLKSMNFDFASSAAF 708

Query: 639 NKSLSK---TGFDDKYSLARKEVLTNMYSRPMQMALLYFCGMLQDQEQRHYALNVPLYT 695
N S+ + TF ++ E+ NM R + A YFC+G ++ + HYAL+ YT
Sbjct: 709 NASMVRLRSTFNEELV----ELFENMAVRSLNRAEYFCTGDFGEKTDWHHYALSFNHYT 763

Query: 696 HFTSPIRRFADVIVHRLAALGYSEQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLF 755
HFTSPIRR+ D+IVHRLL +L + P ++ A HCN+++ S VQE S LF
Sbjct: 764 HFTSPIRYPDIIVHRLLERSLK-NTSPGIDKKNCSLVAAHCNEKKEKSTTVQEDSQQLF 822

Query: 756 FAVLVKE-----SGPLESEAMVMGVLNQAFDVLVLRFGVQKRI 793
+V + E + +A + + DV + +G+ R+
Sbjct: 823 LSVYIAEYCKKHDKKSMPVQAFATRISGNSIDVYISEYGISNRV 866

>gi|15220899|ref|NP_177891.1| putative 3'-5' exoribonuclease; protein id:
At1g77680.1
[Arabidopsis thaliana]
Length = 1055

Score = 414 bits (1063), Expect = e-114
Identities = 277/810 (34%), Positives = 415/810 (51%), Gaps = 78/810 (9%)

Query: 49 IFETYMSKEDVSEGLKRGTLIQGVLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNG 108
IF ++ S + V+E L++G + + R+N +EA+ DI I+G V ++RA+ G
Sbjct: 147 IFSSHWSLDAVTEALEKGEAFKALFRVNAHNRNEAYCKIDGVPTDILINGNVQCQSRAVEG 206

Query: 109 DLVVVKLLPEDQWKAVKPESNDKEIEATYEADIPPEEGCGHHPLQQSRKGWSGPDVIIEAQ 168
D VV+KL P W +K E+ EG P + +K + +
Sbjct: 207 DTVVIKLDPLSLWPKMK-----GFVTESAAKPEGTNSPPEKDDKKARQKNGIDVVEG 258

Query: 169 FDDSDSEDRHGNTSGLVDGVKK-LSISTPDRGKEDSSTPVMKDENTPI PQDTRGLSEKSL 227
F+D S+++ +S + G K ++ S+P + + N G+
Sbjct: 259 FEDGFSKNK---SSVIGKGAKGNGVTPSSPPSLDSCLGSFCEQKGNCSAVDKLCGILSSFP 315

Query: 228 QK--SAKVYYILEKKHSR-AATGILKL---LADKNSDLFK-----KYALFSPSDH 271
K + +VV ++EK R + G+L + + K SD + +Y P+D
Sbjct: 316 HKRPTGQVVAVVEKSLVRDSIVGLLDVKGWIHYKESDPKRCKSPLSLSDEYVQLMPADP 375

Query: 272 RVPRIYVPLKDCPQDFMTRPK----DFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEI 327
R P++ VP P R + + L +I+DW E F + Q+ G+ E+
Sbjct: 376 RFPKLIIVPFHVLPGSIRARLENLDPNLEAELVAAQIVDWGEGSPFPVAQITHLFGRGSEL 435

Query: 328 EPETEGILTEYGVDFSDSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTAR 387
EP+ IL + V SD FS L LP+ +PW +P +EV +R+DLR C+ TIDPSTA D
Sbjct: 436 EPQINAILYQNSVCDSDFSPGSLTSLPR-VPWEVPEEEVQRRKDLRDLCVLTIDPSTATD 494

Query: 388 LDDALACRRLTDGTFEVGVHIADVSYFVPEGSSLKVAERATSVYLVQKVVPMPLPRLLC 447
LDDAL+ + L G F VGVHIADVSYFV ++LD A R+TSVYL+Q+ + MLP LL
Sbjct: 495 LDDALSVQSLPGFFRVGVHIADVSYFVLPETALDTEARFRSTSVDYLMQRKISMLPPLLS 554

Query: 448 EELCSLNPMTDKLTFSVIWKLTPPEGKILEEWFGRTIIRSCTKLSYDHQSMIENXXXXXX 507
E + SL+P D+L FS++W L EG +++ W GRTIIRSC KLSYDHQAQ +I+
Sbjct: 555 ENVGSLSPGADRLAFLSILWDLNREGDVIDRWIGRTIIRSCKLSDHAQDIIDGKSDVAE 614

Query: 508 XXXXXXXXXXXXHSVEVHQAVNLHSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQG 567
+V ++V L I+ LR++RF +GAL+L+ K F D E G+P
Sbjct: 615 NGWPALHGSFKWC-DVTRSVKQLSEISTTLRQKFRNGALQLENSKPVFLFD-EHGVPYD 672

Query: 568 CHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCDQMG 627
+ SN LVEEFMLLANM A I + + +LLRRHP P T+ L + FC + G
Sbjct: 673 FVTCSRKGSNFLVEEFMLLANMTAAEVISQAYRASSLLRRHPEPNTRKLKEFEGFCSKHG 732

Query: 628 LPMDVSSAGALNKSLTKTFGDDKYSLARKEVLTNMYSRPMQMAYFCGMLQDQ-EQFRH 686
+ +D+SS+G L SL K G+ K ++L N +PMQ+A YFC+G L+D ++ H
Sbjct: 733 MDLDIISSGQLQDSLEKITGNLKDDSVFVDILNNYAIKPMQLASYFCTGNLKDSVAEWH 792

Query: 687 YALNVPLYTHFTSPIRFADVIVHR----LLAAALGYSEQPDVEPD----- 728
YAL VPLYTHFTSP+RR+ D++VHR L A YS+Q D
Sbjct: 793 YALAVPLYTHFTSPLRRYPDIVVHRALAALEAEELYSKQKQTAIDEGRSCFTGIHFNKD 852

Query: 729 -----TLQKQADHCNDRRMASKRVQELSIGLFFAVLVKESG 764
L A +CN+R++A+++V++ L+ ++K+
Sbjct: 853 AAESIEGKEALSAALKHGPSTEILSDVAAYCNERKLAARKVARDACDKLYTWFVLKQKE 912

Query: 765 PLESEAMVMGVLNQAFDVLVLRFGVQKRIY 794
EA VM + ++ V + + G+++RIY
Sbjct: 913 IFPCEARVMNLGSRFMTVYISKLGIERRIY 942

>gi|25406521|pir||E96806 hypothetical protein T32E8.1 [imported] -
Arabidopsis thaliana
gi|12323300|gb|AAG51632.1|AC012193_14 putative 3'-5' exoribonuclease, 3'
partial; 3320-1 [Arabidopsis
thaliana]
Length = 935

Score = 402 bits (1033), Expect = e-110
Identities = 274/792 (34%), Positives = 404/792 (51%), Gaps = 80/792 (10%)

Query: 49 IFETYMSKEDVSEGLKRGTЛИQGVLRINPKKFHEAFIPS PGDRDIFIDGVVARNRALNG 108
IF ++ S + V+E L++G + + R+N +EA+ DI I+G V ++RA+ G
Sbjct: 147 IFSSHWSLDAVTEALEKGEAFKALFRVNAHNRNEAYCKIDGVPTDILINGNVCQSRAVEG 206

Query: 109 DLVVVKLLPEDQWKAVKPESNDKEIEATYEADIP EEGCGHHPLQOSRKGWSGPDVII EAQ 168
D VV+KL P W +K E+ EG P + +K + +
Sbjct: 207 DTVVIKLDPLSLWPKMK-----GFVTESA AKPEGTNSPPEKDDKKARQKNGIDVVEG 258

Query: 169 FDDSDSED RHGNTSGLVDGVKK-LSISTPDRGKEDSSTPVMKDENTPI PQDTRGLSEKSL 227
F+D S+++ +S + G K ++ S+P + + N G+
Sbjct: 259 FEDGFSKNK---SSVIGKGAKNGVTPSSPPSLSDCLGSFCEQKGNCSAVDKLCGILSSFP 315

Query: 228 QK--SAKVVYILEKKHSR-AATGILKL---LADKNSDLFK-----KYALFSPSDH 271
K + +VV ++EK R + G+L + + K SD + +Y P+D
Sbjct: 316 HKRPTGQVVA VVEKSLVRDSIVGLLDVKGWIHYKESDPKRCKSPLSLSDDEYVQLMPADP 375

Query: 272 RVPRIYVPLKDCPQDFMTRPK---DFANTLFICRIIIDWKEDCNFALGQLAKSLGQAGEI 327
R P++ VP P R + + L +I+DW E F + Q+ G+ E+
Sbjct: 376 RFPKLIVPFHVLPGSIRARLENLDPNLEAEELVAAQIVDWGEGSPFPVAQITHLFGRGSEL 435

Query: 328 EPETEGILTEYGVDFSDSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARD 387
EP+ IL + V SDFS L LP+ +PW +P +EV +R+DLR C+ TIDPSTA D
Sbjct: 436 EPQINA ILYQNSVCDSDFSPGSLTSLPR-VPWEVPEEEVQRRKDLRDLCVLTIDPSTATD 494

Query: 388 LDDALACRRLTDGTFEVGVHIADVSYFVPEGSSL DKVAAERATSVYLVQKVVPMLPRLLC 447
LDDAL+ + L G F VGVHIADVSYFV ++LD A R+TSVYL+Q+ + MLP LL
Sbjct: 495 LDDALSVQSLPGGFFRVGVHIADVSYFVL PETALDTEARFRSTS VYLMQRKISMLPPLLS 554

Query: 448 EELCSLNPM TDKLTF SVIWKLTPEGKILEEWFGRTIIRSCTKLSYDHAQSMIENXXXXXX 507
E + SL+P D+L FS++W L EG + + W GRTIIRSC KLSYDHAQ +I+
Sbjct: 555 ENVGSLSPGADRLA FSI LWDLNREGDV IDR WIGRTIIRSCCKL SYDHAQDIIDGKSDVAE 614

Query: 508 XXXXXXXXXXXXHSVEEVHQAVNLHSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQG 567
+V ++V L I+ LR++RF +GAL+L+ K F D E G+P
Sbjct: 615 NGWPALHGSFKWC-DVTRSVKQLSEISTTLRQKFRNGALQLENSKPVFLFD-EHGVPYD 672

Query: 568 CHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQT KMLSDLVEFCDQMG 627
+ SN LVEEFML LANM A I + + +LLRRHP P T+ L + FC + G
Sbjct: 673 FVTCSRKGSNFLVEEFML LANMTAAEVISQAYRASSLLRRHPEPNTRKLKEFEGFCSKHG 732

Query: 628 LPMDVSSAGALNKS LT KTFGDDKYS LARKEVLT NMYSRPMQM ALYFC SGMLQDQ-EQFRH 686
+ +D+SS+G L SL K G+ K ++L N +PMQ+A YFC+G L+D ++ H
Sbjct: 733 MDLDI SSSGQLQDSLEKITGNLKDDSVFVDILNNYAIKPMQLASYFCTGNLKDSVAEWH 792

Query: 687 YALNVPLYTHFTSPIRFADVIVHR---LLAAALGYSEQPDVEPD----- 728
YAL VPLYTHFTSP+RR+ D++VHR L A YS+Q D
Sbjct: 793 YALAVPLYTHFTSPLRRYPDIVVHRA LAALEAEELYSKQKQTAIDEGRSCFTGIHF NKD 852

Query: 729 -----TLQKQADHCNDRRMASKRVQELS IGLF--FAVLVKE 762
L A +CN+R++A+++V++ L+ F + KE
Sbjct: 853 AAESIEGKEALSVAALKHGPSTEILSDVAAYCNERKLAARKVRDACDKLYTWFVLKQKE 912

Query: 763 SGPLESEAMVMG 774
P E+ M +G
Sbjct: 913 IFPCEARVMNLG 924

>gi|25332397|pir||A84553 probable mitotic control protein dis3 [imported] -
Arabidopsis
 thaliana
 Length = 955

Score = 396 bits (1018), Expect = e-109
Identities = 252/757 (33%), Positives = 407/757 (53%), Gaps = 84/757 (11%)

Query: 49 IFETYMSKEDVSEGLKRGTЛИQGVLRINPKKFHEAFIPSPDGRDIFIDGVVARNRALNG 108
I++ + +++ GL RG QG LR+N +EA++ S +I I G NRA +G
Sbjct: 215 IYQEHKPMSEITAGLHRGIYHQGKLRVNRFNPYEAYVGSESIGEEIIIYGRSNMNRADF 274

Query: 109 DLVVVKLLPEDQWKAVKPESNDKEIEATYEADIPEEGCGHPLQQSRKGWSPDVIIEAQ 168
D+V V+LLP DQW+ ++K + EA I S DV++
Sbjct: 275 DIVAVELLPRDQWQ-----DEKALSIAEEAVI-----SLHDVVLNLS 311

Query: 169 F---DDSDSEDRHGNTSGL---VDGVKKLSISTPDRGKEDSSTPVMKDENTPIQDTRG 221
F +S+++D +T L VD + S + + + ++ PV
Sbjct: 312 FFQISNSNADDEEDDTVHLAPDNVDDAPRTSNLSHETSGDKNAAPV----- 357

Query: 222 LSEKSLQKSAKVVYILEKKHSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLK 281
+ S +VV ++ +++ + G L+ ++ +ALF D R+P+I + +
Sbjct: 358 -----RPSGRVVGVI-RRNWHSYCGSLEPMSLPAGSGGTAHALFVSKDRRIPKIRINTR 410

Query: 282 DCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGV 341
++ + + + W + G + +G+ G+ E ETE +L E VD
Sbjct: 411 QL-----QNLLDMRIVVAVDSWDRQSRYPGHSYVRPIKGKIGDKETETEVVLIENDVD 462

Query: 342 FSDFSSEVLECLPQSLPWTIPPDEVGK--RRDLRKDCIFTIDPSTARLDLACRRLTD 399
+S FSS+VL CLP LPW++ ++V R+DLR +F++DP +D+DDAL C L +
Sbjct: 463 YSPFSSQVLAQCLP-PLPWSVSSEDVSNPVRQDLRHLLVFSVDPPGCKDIDDALHCTSLPN 521

Query: 400 GTFEVGVHIADVSYFPEGSSLKDVAERATSVYLVQKVVPMPLPRLLCEELCSLNPMTDK 459
G FE+GVHIADV+ FV G+ LD A++R TSVYLV++ + MLP+ L E++CSL ++
Sbjct: 522 GNFELGVHIADVTNFVHPGTPLDDEASKRGTSVYLVERRIDMLPKPLTEDICSLRADVER 581

Query: 460 LTFSVIWKLTPEGKILEEWFGRTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXHS 519
L FSVIW+++P+ +I+ F ++II+S LSY AQ+ ++
Sbjct: 582 LAFSVIEMSPDAEIISTRFTKSIIKSSAALSYIEAQARMDDSRL----- 626

Query: 520 VEEVHQAVLNLSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKL 579
+ + + N+++AK +R++R GAL L ++ F +D E P +Y+ ++N++
Sbjct: 627 TDSLTTDLRNMNTLAKIMRQRRIDRGALTASAEVKFDIDPENHDPLNIGMYQILEANQM 686

Query: 580 VEEFMLLANMAVAHKIFRTFPEQALLRRHPPQTKMLSDLVEFCDQMGPMVDVSSAGALN 639
VEEFML AN++VA +I + FP +LLRRHP P +ML L+ +GL +DVSS+ AL
Sbjct: 687 VEEFMLAANVSVAGQILKLFPSCSLLRRHPTPTREMLEPLLRTAAIGLTLVDSSSKALA 746

Query: 640 KSLTKTFGDDKYSLARKEVLTNMYSRPMQMALYFCGMLQDQEQRHYALNVPLYTHFTS 699
SL + G+D Y +++ + +R M A+YFCGS L E + HY L PLYTHFTS
Sbjct: 747 DSLDRAVGEDPYF---NKLIRILATRCMTQAVYFCSGDLSPP-EYHYGLAAPLYTHFTS 802

Query: 700 PIRRFAVIVHRLAALGYSEQPDVEPD--TLQKQADHCNDRRMASKRVQELSIGLFFA 757
PIRR+ADV VHRLAALGYSEQPDVEPD--TLQKQADHCNDRRMASKRVQELSIGLFFA 757
Sbjct: 803 PIRRYADVFVHRLAASLGIYKLPTVFQDRPQLTSVADNLNYRHRNAQMAGRASVELYVL 862

Query: 758 VLVKESGPLSEAMVMGVLNQAFDVLVLRFGVQKRIY 794
+ + + P + EA V+ + + F V V ++G++ +Y
Sbjct: 863 IYFR-TRPTDEEARVVKIRSNGFIVFVPKYGIEGPVY 898

>gi|24654592|ref|NP_728490.1| CG16940-PC [Drosophila melanogaster]
gi|23092667|gb|AAN11425.1|AE003467_37 CG16940-PC [Drosophila melanogaster]
Length = 1044

Score = 367 bits (942), Expect = e-100
Identities = 249/739 (33%), Positives = 372/739 (50%), Gaps = 82/739 (11%)

Query: 66 GTLIQGVLRINPKKFHEAFIPSPGDGRDIFIDGV---VARNRALNGDLVVVKLL-PEDQ 120
G +++ +R+N K +AFI + DG+ VAR A +GD V +L P Q
Sbjct: 308 GRIVEEEIRVNRKNNRQAFIIMSTDREALERDGIVLLPVARRYAFDGDKVRAFVLNPGAQ 367

Query: 121 WKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSGPDVIIEAQFDDSDSEDRHGN 180
+ E + EI G P G E DD++S+ +
Sbjct: 368 GSSKTAEPSSGEIS-----GGKPSLSSLADG-----EELSDDTESQGSESD 407

Query: 181 TSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIQPQDTRGLSEKSLQKSAKVVYILEKK 240
T +V V+ +N P A V+ I ++
Sbjct: 408 TDNVV-----VISSDNCP-----KAFVIAITKRT 431

Query: 241 HSRAATGIL-----KLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFMTRPK-D 293
R G + KL D+ LF K F P D RVP +YVP C + + D
Sbjct: 432 ELRQIVGTISFTNPTKLCDDQ---LFYK---FRPYDLRVPMVYVPKDACAHHIGNKQQID 485

Query: 294 FANTLFICRIIDWKEDCN-FALGQLAKSLGQAGEIEPETEGILTEYGV-DFSDFSSEVLE 351
+ L++ I++ DCN + +L + +G+ G ++ E + IL G+ D F ++
Sbjct: 486 VSGLLYLAHILE--TDCNGHCIAELIQPVGRVGNLDDELKAILFHNGLRDIKPFEQRFD 543

Query: 352 CLPQSLPWTPDEVGKRRDLRKDCIFTIDPSTARLDDALACRRLTDGTFEVGVHIADV 411
Q P I +++ +R+DLRK CIFTIDP TARLDDA++ +L D +E+GVHI+DV
Sbjct: 544 IYSQPPP-PISQEDLRQRKDLRKMCIFTIDPMTARLDDAVSIEKLGDNEYEIGVHISDV 602

Query: 412 SYFVPEGSSLDKVAEARATSVYLVQKVVPMPLRPLLCEELCSLNPMTDKLTFSVIWKLTPE 471
S+F+ E + LD + ER+TS+YL +V+ MLP+ LC CSL P DK FSV W++ +
Sbjct: 603 SHFLIEDNELDNIVKERSTSIYLANEVIHMLPQSLCMR-CSLLPGQDKFAFSVFWRMNGK 661

Query: 472 GKILEE--WFGRTIIRSCTKLSYDHQSMEIENXXXXXXXXXXXXHSVEEVHQAVLN 529
G +L++ F RT+I SC++ +Y+HAQ +I+N + + + VL
Sbjct: 662 GVMLQKKPEFCRTVINSCSQFAYEHAQKIIDNPNERFTENDFPTILNGFPDDIRNRVLW 721

Query: 530 LHSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANM 589
LH IA +R+ R +GAL ++ KL F LD TG P + + R++N+L+EEFMLLAN
Sbjct: 722 LHDIASSIRKTRLNGALTINNAKLRFLLDPITGEPLSFEVEKQREANRLIEEFMLLANQ 781

Query: 590 AVAHKIFRTFPEQALLRRHPPQTCKMLSDLVEFCDQMGLPMVDVSSAGALNKS LT KTFGDD 649
AVA I +FP+ A+LR HPPP K L L E +G +D SS+ AL +S+ + +
Sbjct: 782 AVARFIHDSFPDIAVLRNHPPPLIKSLKALREKLLALGFELDYSSSKALQESMVRLCNEA 841

Query: 650 KYSLARKEVLTNMYSRPMQMALYFCGMLQDQEQRHYALNVPLYTHFTSPIRFADIV 709
+A L+ + +PM A YFCS + HYAL++P+YTHFTSPIRR+ D++V
Sbjct: 842 PNPVAMNACLSQLLMKPMARATYFCSEGKSEPADLWHYALSIPIYTHFTSPIRYPDILV 901

Query: 710 HRLLAAALGYSEQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVLVKESGPLSE 769
HRLLAAAL Y P PD L N+R+ +K+ E S L+F V +
Sbjct: 902 HRLLAAALKYCTPPKRTPDDLHTLTKLANERKYNACKAGEDSGNLYFKRYVHNKQGIYMR 961

Query: 770 AMVMGVLNQAFDVLVLRFG 788
A+V+ + +V+ L G
Sbjct: 962 AVVIEIFQHMMNVVTLESG 980

>gi|19922976|ref|NP_612012.1| CG16940-PA [Drosophila melanogaster]
gi|24654597|ref|NP_728491.1| CG16940-PB [Drosophila melanogaster]
gi|16198179|gb|AAL13898.1| LD37985p [Drosophila melanogaster]
gi|23092668|gb|AAF47351.2| CG16940-PA [Drosophila melanogaster]
gi|23092669|gb|AAN11426.1|AE003467_39 CG16940-PB [Drosophila melanogaster]
Length = 1032

Score = 367 bits (942), Expect = e-100
Identities = 249/739 (33%), Positives = 372/739 (50%), Gaps = 82/739 (11%)

Query: 66 GTLIQGVLRINPKKFHEAFIPSPDGDRDIFIDGV---VARNRALNGDLVVVKLL-PEDQ 120
G +++ +R+N K +AFI + DG+ VAR A +GD V +L P Q
Sbjct: 296 GRIVEEEIRVNRKNNRQAFIIMSTDREALERDGIVLLPVARRYAFDGDKVRAFVLNPQAQ 355

Query: 121 WKAVKPESNDKEIEATYEADIPPEEGCGHHPLQQSRKGWSGPDVIIIEAQFDDSDSEDRHGN 180
+ E + EI G P G E DD++S+ +
Sbjct: 356 GSSKTAEPSSGEIS-----GGKPSLSSLADG-----EELSDDTESQGSESD 395

Query: 181 TSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIQPQDTRGLSEKSLQKSAKVVYILEKK 240
T +V V+ +N P A V+ I ++
Sbjct: 396 TDNVV-----VISSDNCP-----KAFVIAITKRT 419

Query: 241 HSRAATGIL-----KLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFMTRPK-D 293
R G + KL D+ LF K F P D RVP +YVP C + + D
Sbjct: 420 ELRQIVGTISFTNPTKLCDDQ---LFYK---FRPYDLRVPVMVYVPKDACAHHIGNKQQID 473

Query: 294 FANTLFICRIIIDWKEDCN-FALGQLAKSLGQAGEIEPETEGILTEYGV-DFSDFSSEVLE 351
+ L++ I++ DCN + +L + +G+ G ++ E + IL G+ D F ++
Sbjct: 474 VSGLLYLAHILE--TDCNGHCIAELIOPVGRVGNLDDELKAILFHNGLRDIKPFEQRFD 531

Query: 352 CLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARLDLACRRLTDGTFEVGVHIADV 411
Q P I +++ +R+DLRK CIFTIDP TARLDLDA++ +L D +E+GVHI+DV
Sbjct: 532 IYSQPPP-PISQEDLRQRKDLRKMCIFTIDPMTARDLDDAVSIEKLGDNYEIGVHISDV 590

Query: 412 SYFVPEGSSLDKVAEAERATSVLVQKVVPMPLPRLLCEELCSLNPMTDKLTFSVIWKLTP 471
S+F+ E + LD + ER+TS+YL +V+ MLP+ LC CSL P DK FSV W++ +
Sbjct: 591 SHFLIEDNELDNIVKERSTSIIYLANEVIHMLPQSLCMR-CSLLPGQDKFAFSVFWRMNGK 649

Query: 472 GKILEE--WFGRTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXHSVEEVHQAVLN 529
G +L++ F RT+I SC++ +Y+HAQ +I+N + + + VL
Sbjct: 650 GVMLQKKPEFCRTVINSCSQFAYEHAQKIIDNPNERFTENDFPTILNGFPDDIRNRVLW 709

Query: 530 LHSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANM 589
LH IA +R+ R +GAL ++ KL F LD TG P + + R++N+L+EEFMLLAN
Sbjct: 710 LHDIASSIRKTRLNGALTINNAKLRFLLDPTGEPLSFEVEKQREANRLIEEFMLLANQ 769

Query: 590 AVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKS LT KTFGDD 649
AVA I +FP+ A+LR HPPP K L L E +G +D SS+ AL +S+ + +
Sbjct: 770 AVARFIHDSFPDIAVLRNHPPPLIKSLKALREKLLALGFELDYSSSKALQESMVRLCNEA 829

Query: 650 KYSLARKEVLTNMYSRPMQMAMYFCGMLQDQEQRHYALNVPLYTHFTSPIRFADVIV 709
+A L+ + +PM A YFCS + HYAL++P+YTHFTSPIRR+ D++V
Sbjct: 830 PNPVAMNACLSQLLMKPMARATYFCSEGKSEPADLWHYALSIPIYTHFTSPIRYPDILV 889

Query: 710 HRLLAAALGYSEQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVLVKESGPLESE 769
HRLLAAAL Y P PD L N+R+ +K+ E S L+F V +
Sbjct: 890 HRLLAAALKYCTPPKRTPDDLHTLTKLANERKYNACKAGEDSGNLYFKRYVHNKQGIYMR 949

Query: 770 AMVMGVLNQAFDVLVLRFG 788
A+V+ + +V+ L G
Sbjct: 950 AVVIEIFQHMMNVVTLESG 968

>gi|15292611|gb|AAK93574.1| SD10981p [Drosophila melanogaster]
Length = 982

Score = 351 bits (901), Expect = 2e-95
Identities = 249/815 (30%), Positives = 407/815 (49%), Gaps = 110/815 (13%)

Query: 50 FETYMSKEDVSEGLKRGTLIQQVLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNGD 109
+ ++S +++ EGL++ L+QG + + + + E + + + I I G + NRA++GD
Sbjct: 232 YPPHLSMKELLEGRLQNKLLOQTFQASRENYLEGTVNVEKFEKGILIQGRESLNRAVDGD 291

Query: 110 LVVVKLLPEDQWKAVKPESNDKEIEATYEADIPPEEGCGHHPLQQSRKGWSGPDVIIIEAQF 169
LV V+LLPE +W A P E + Y ++P
Sbjct: 292 LVAVELLPEAEWSA--PSEIVLEEKNVYADEVP----- 322

Query: 170 DDSDSEDRHGNTSGLVKKLSISTPDRGKEDSSTPVMKDENTPIPQDTRGLSEKSLQK 229
SE+R + + +++ V+ ++S E TP
Sbjct: 323 ---SEERAKDENEMLNQVRAAALSA-----ERTP----- 348

Query: 230 SAKVYYILEKKHSRAATGILK--LLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDF 287
+ ++V I+ +K R GIL+ L+ D N +F P+D ++PRI + +
Sbjct: 349 TGRIVGIVRRKW-RQYCGILQPSLIEDTNRH-----IFVPADRKİPRIRIETRQAAM-- 399

Query: 288 MTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSS 347
N I I W + + G +SLG G++ E E IL E+ V FS
Sbjct: 400 -----LQNQRIIIVTIDTWPRNSRYPHGFVRSLGPLGDMATENEVILLEHDVPHCKFSD 453

Query: 348 EVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARLDALACRRLTDGTFEVGVH 407
EVL LP+ +PWTI ++ KR DLR I ++DP D+DDAL CR L +G EVGVH
Sbjct: 454 EVLSFLPK-MPWTITDEDYSKRVDLRDLYICSVDPGCTDIDDALHCRELPGNLEVGVH 512

Query: 408 IADVSYFVPEGSSLKDVAERATSVYLVQKVVPMPLRPLLCEELCSLNPMTDKLTFSVIWK 467
IADVS+F+ G++LD AA R T+VYLV K + M+P LL LCSL ++ FS +W+
Sbjct: 513 IADVSHFIRPGNALDMEAARGTTVYLVGKRIDMVPPELLSNLCSLVGGVERFAFSCVWE 572

Query: 468 LTPEGKILEEWFGRTIIRSCTKLSYDHQSMEIENXXXXXXXXXXXXHSVEEVHQAV 527
+ E +L + F ++I+S ++Y+ AQ++I++ E+ +++
Sbjct: 573 VDNEANVLSKRFHKSVIKSKRAMTYEEAQNIIDDATQQ-----NEIAKSL 617

Query: 528 LNLHSIAKQLRRQRFDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLA 587
NL+ +AK L+++R +GAL L ++ F +D ET P + + R++N +VEEFMLLA
Sbjct: 618 RNLNRLAKILKKRMDNGALVLASPEIRFQVDSETHEPLEVEVKQMRETNSMVEEFMLLA 677

Query: 588 NMAVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKS LTKF- 646
N+ VA I F E A+LRRHP P LV+ G +D++S L+ SL K
Sbjct: 678 NITVAEHIAATEFSECAVLRRHPRPPPTNFDPLVKSARYQGFQVDINSGLELSHSLDKCVK 737

Query: 647 GDDKYSLARKEVLTNMYSRPMQMALYFCGMLQDQEQRHYALNVPLYTHFTSPIRRFAD 706
D+ Y +LT +R M A+YF SG LQ +E+F HY L P+YTHFTSPIRR++D
Sbjct: 738 ADNPYFNTMIRILT---TRCMMQAVYFISGSLQ-KEEFFHYGLAAPIYTHFTSPIRRYSD 793

Query: 707 VIVHRLAALG---YSEQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVLVKE 762
++VHRLAALG++G Y++ D + + ++ + N R ++ S+ L + +
Sbjct: 794 IMVHRLAASIGADSTYAQLLDRKSN--EELCHNLNYRHKAQYAGRASVALNTHLFFRG 851

Query: 763 SGPLESEAMVMGVLNQAFDVLVLRFGVQKRIYCNALALRSYSFQKVGKKPELTLVWEPPD 822
+ E V+ V A VL+ ++G++ +Y + ++V K E+ + +D
Sbjct: 852 KEE-DEEGYVLFVRKNALQVLIPKYGLEGTLYLKSDKDGKDGVERV--KSEIVFTFNEED 908

Query: 823 LEEEPTQQVITIFSLVDVVLQAEATALKYSAILKR 857
+ V F V V L + + + + + R
Sbjct: 909 HTQRCGDVVFHSFDPVTVRLSLDSSNVQHEKLIFR 943

>gi|18488261|ref|XP_081229.1| Dis3 [Drosophila melanogaster]
gi|24649634|ref|NP_651246.2| CG6413-PA [Drosophila melanogaster]
gi|7301148|gb|AAF56281.1| CG6413-PA [Drosophila melanogaster]
Length = 982

Score = 350 bits (898), Expect = 6e-95
Identities = 248/815 (30%), Positives = 407/815 (49%), Gaps = 110/815 (13%)

Query: 50 FETYMSKEDVSEGLKRGTLIQGVLRINPKKFHEAFIPS PGDRDIFIDGVVARNRALNGD 109
+ ++S +++ EGL++ L+QG + + + E + ++ I I G + NRA++GD
Sbjct: 232 YPPHLSMKELLEGRLQNKLLQGTFQASRENYLEGTVNVEKFEKGILIQGRESLNRAVDGD 291

Query: 110 LVVVKLLPEDQWKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSGPDVIIEAQF 169
LV V+LLPE +W A P E + Y ++P
Sbjct: 292 LVAVELLPEAEWSA--PSEIVLEEKNVYADEVP----- 322

Query: 170 DDSDSEDRHGNTSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIQPQDTRGLSEKSLQK 229
SE+R + + +++ V+ ++S E TP
Sbjct: 323 ---SEERAKDENEMLNQVRAAALSA-----ERTP----- 348

Query: 230 SAKVYYILEKKHSRAATGILK--LLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDF 287
+ ++V I+ +K R GIL+ L+ D N +F P+D ++PRI + +
Sbjct: 349 TGRIVGIVRRKW-RQYCGILQPSLIEDTNRH-----IFVPADRKPRIKIRIETRQAAM- 399

Query: 288 MTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSS 347
N I I W + + G +SLG G++ E E IL E+ V FS
Sbjct: 400 -----LQNQRIIIVTIDTWPRNSRYPHGHFVRSLGPLGDMATENEVILLEHDVPHCKFSD 453

Query: 348 EVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARLDLACRRLTDGTFEVGVB 407
EVL LP+ +PWTI ++ KR DLR I ++DP D+DDAL C+ L +G EVGVH
Sbjct: 454 EVLSFLPK-MPWTITDEDYSKRVDLRDLYICSVDPNGCTDIDDAHLCKELPNGNLEVGVB 512

Query: 408 IADVSYFVPEGSSLDKVAERATSVYLVQKVVPMPLRLLCEELCSLNPMTDKLTFSVIWK 467
IADVS+F+ G++LD AA R T+VYLV K + M+P LL LCSL ++ FS +W+
Sbjct: 513 IADVSHFIRPGNALDMEAARGTTVYLVGKRIDMVPPELLSSNLCSLVGGVERFAFSCVWE 572

Query: 468 LTPEGKILEEWFGRTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXHSVEVHQAV 527
+ E +L + F +++I+S ++Y+ AQ++I++ E+ +++
Sbjct: 573 VDNEANVLSKRFHKSVIKSKRAMTYEEAQNIIDDATQQ-----NEIAKSL 617

Query: 528 LNLHSIAKQLRRQRFDVGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLA 587
NL+ +AK L+++R +GAL L ++ F +D ET P + + R++N +VEEFMLLA
Sbjct: 618 RNLNRLAKILKKRMDNGALVLASPEIRFQVDSETHEPLEVEVKQMRETNSMVEEFMLLA 677

Query: 588 NMAVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKSLTKF- 646
N+ VA I F E A+LRRHP P LV+ G +D++S L+ SL K
Sbjct: 678 NITVAEHIAATEFSECABLRRHPRPPPTNFDPLVKSARYQGFQVDINSGLELSHSLDKCVK 737

Query: 647 GDDKYSLARKEVLTNMYSRPMQMAYFCGMLQDQEQRHYALNVPLYTHFTSPIRRFAD 706
D+ Y +LT +R M A+YF SG LQ +E+F HY L P+YTHFTSPIRR++D
Sbjct: 738 ADNPYFNTMIRILT---TRCMMQAVYFISGSLQ-KEEFFHYGLAAPIYTHFTSPIRRYSD 793

Query: 707 VIVHRLLAALG---YSEQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVLVKE 762
++VHRLLA++G Y++ D + + ++ + N R ++ S+ L + +
Sbjct: 794 IMVHRLLAASIGADSTYAQLLDRKSN--EELCHNLNYRHMAQYAGRASVALNTHLFFRG 851

Query: 763 SGPLESEAMVMGVLNQAFDVVLRLFGVQKRIYCNALALRSYSFQKVGKKPELTLVWEPPD 822
+ E V+ V A VL+ ++G++ +Y + ++V K E+ + +D
Sbjct: 852 KEE-DEEGYVLFVRKNALQVLIPKYGLEGTLYLKSDKDGKDGVERV--KSEIVFTFNEED 908

Query: 823 LEEEPTQQVITIFSLVDVVLQAEATALKYSAILKR 857
+ V F V V L +++ +++ ++ R
Sbjct: 909 HTQRCGDDVFHSFDPVTVRLSLDSSNVQHEKLIFR 943

>gi|21748526|dbj|BAC03400.1| FLJ00327 protein [Homo sapiens]
Length = 266

Score = 343 bits (879), Expect = 9e-93
Identities = 167/188 (88%), Positives = 175/188 (93%)

Query: 578 KLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGA 637
+LVEEFMLLANMAVAHKI R FPEQALLRRHPPPQT+MLSDLVEFCDQMGLP+D SSAGA
Sbjct: 29 RLVEEFMLLANMAVAHKIHRAFPEQALLRRHPPPQTMLSDLVEFCDQMGLPVDFSSAGA 88

Query: 638 LNKSLLTGFDDKYSLARKEVLTNMYSRPMQMAYFCGMLQDQEQRHYALNVPLYTHF 697
LNKSLLT+TGFDDKYSLARKEVLTNM SRPMQMAYFCG+LQD QFRHYALNVPLYTHF
Sbjct: 89 LNKSLLTGFDDKYSLARKEVLTNMCSRPMQMAYFCGLLQDPAQFRHYALNVPLYTHF 148

Query: 698 TSPIRRFADVIVHRLLAALGYSEQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFA 757
TSPIRRFADV+VHRLLAALGY E+ D+ PDTLQKQADHCNDRRMASKRVQELS LFFA
Sbjct: 149 TSPIRRFADVVLVHRLLAALGYRERLDMAPDTLQKQADHCNDRRMASKRVQELSTSLFFA 208

Query: 758 VLVKESGP 765

VLVK S P

Sbjct: 209 VLVKVSP 216

>gi|26327903|dbj|BAC27692.1| unnamed protein product [Mus musculus]
Length = 687

Score = 340 bits (871), Expect = 7e-92

Identities = 233/670 (34%), Positives = 344/670 (51%), Gaps = 60/670 (8%)

Query: 192 SISTPDRGKEDSSTPVMKDENTPI PQDTRGLSEKSLQSAKVVYILEKKHSRAATGILKL 251
S+ D G+ + V KDE + T +SEK L+ + +VV I+ K++ R G+L

Sbjct: 36 SVVLDDEGQNEDD--VEKDEERELLKT-AVSEKMLRPTGRVVGII-KRNWRPYCGMLSK 91

Query: 252 LADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFMTRPKDFANTLFICRIIDWKEDCN 311
K S + LF+P+D R+PRI + + + I I W +

Sbjct: 92 SDIKES---RRHLFTPADKRIPRIRIETR-----QASALEGRRIIVAIIDGWPRNSR 139

Query: 312 FALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPWTIPPDEVGKRRD 371
+ G K+LG GE E ETE +L E+ V FS VL LP+ +PW+I +++ R D

Sbjct: 140 YPNGHFVKNLGDVGEKETETEVLLLEHDVPHQPFSAVLSFLPR-MPWSITEEDMKNRED 198

Query: 372 LRKDCIFTIDPSTARLDALACRRLTDGTFEVGVHIADVSYFVPEGSSLKDVAERATS 431
LR C+ ++DP D+DDAL CR L++G EVGVHIADVS+F+ G++LD+ +A R T+

Sbjct: 199 LRHLCVCSVDPGCTDIDDALHCRELNGNLEVGVHIADVSHFIRPGNALDQESARRGTT 258

Query: 432 VYLVQKVVPMPLPRLLCEELCSLNPMTDKLTFSVIWKLTPEGKILEEWFGRTIIRSCTKLS 491
VYL +K + M+P LL LCSL D+L FS IW++ +IL+ F +++I S L+

Sbjct: 259 VYLCEKRIDMVPELLSSNLCSLRNSNDLAFSCIWEMNHNAEILKTRFTKSVINSKASLT 318

Query: 492 YDHAQSMIENXXXXXXXXXXXXXXHSVEEVHQAVLNLSIAKQLRRQRFDGALRLDQ 551
Y AQ I++ +++ ++ L+ +AK L++ R GAL L

Sbjct: 319 YAEAQMRIDSAAMN-----DDITTSLRGLNQLAKILKKGRIEKGALTSS 363

Query: 552 LKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPP 611
++ F +D ET P E R++N +VEEFMLLAN++VA KI F E ALLR+HP P

Sbjct: 364 PEIRFHMDSETHDPIDLQTKELRETNSMVEEFMLLANISVAKKIHEEFSEHALLRKHPAP 423

Query: 612 QTKMLSDLVEFCDQMGLPMVDVSSAGALNKS LT KTFGDDKYSLARKEVLTNMYSPRMQMAL 671
LV+ L + +A +L SL + D L +L + +R M A+

Sbjct: 424 PPSNYDILVKAAKSKNLQIKTDTAKSLADSLDRAESPDPYLY--NTLLRILATRCMMQAV 481

Query: 672 YFCGMLQDQEQRHYALNVPLYTHFTSPIRFAADVIVHRLAALG---YSEQPDVEP 727
YFCGML D F HY L P+YTHFTSPIR+AD+IVHRLA A+G Y E D

Sbjct: 482 YFCGMDND---FHHYGLASPIYTHFTSPIRRYADIIVHRLAIGADCTYPELTDK-- 536

Query: 728 DTLQKQADHC---NDRRMASKRVQELSIGLFFAVLVKESGPLSEAMVMGVLNQAFDV LV 784
K +D C N R ++ Q S+ + K G + EA ++ V A VL+

Sbjct: 537 ---HKLSDICKNLNFRHKMAQYAQRAVAFHTQLFFSKSGIVSEEAYILFVRKNAAIVVLI 593

Query: 785 LRGVQKRIYCNALALRSYSFQKVGKKPELTLVWEPPDDLEEEPTQQVITIFSLVDVVLQA 844
++G++ ++ +K KP L E L E T V +F V V +

Sbjct: 594 PKYGLETVFFE-----EKDKPKPRLAYDEIPSLRIEGT--VFHVFDKVVKVKITL 642

Query: 845 EATALKYSAI 854

+++ L++ I

Sbjct: 643 DSSNLQHQKI 652

Score = 37.7 bits (86), Expect = 0.87

Identities = 20/54 (37%), Positives = 32/54 (59%), Gaps = 2/54 (3%)

Query: 91 DRDIFIDGVVARNRALNGDLVVVKLLPEDQWKAVKPESNDKEIEATYEADIPEE 144

+++I I G+ NRA++ D+V V+LLP QW V P S + E E D+ ++

Sbjct: 1 EKEILIQGIKHLNRAVHEDIVAVELLPRSQW--VAPSSVVLDDEGQNEDDVEKD 52
 >gi|13446610|emb|CAC35051.1| putative exoribonuclease DIS3 [Drosophila melanogaster]
 Length = 983

 Score = 335 bits (859), Expect = 2e-90
 Identities = 244/816 (29%), Positives = 401/816 (49%), Gaps = 111/816 (13%)

 Query: 50 FETYMSKEDVSEGLKRGTLIQQVLRINPKKFHEAFIPSPDGDRDIFIDGVVARNALNGD 109
 + ++S +++ EGL++ L+QG + + + + E + + + I I G + NRA++GD
 Sbjct: 232 YPPHLSMKELLEGRLRQNKLQLQGTFOASRENYLEGTVNVEKFEKGILIQGRESLNRAVDGD 291

 Query: 110 LVVVKLLPEDQWKAVKPESNDKEIEATYEADIPPEEGCGHHPLQQSRKGWSGPDVIIEAQF 169
 LV V+LLPE +W A P E + Y ++P
 Sbjct: 292 LVAVELLPEAEWSA--PSEIVLEEKNVYADEVP----- 322

 Query: 170 DDSDSEDRHGNTSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIQPQDTRGLSEKSLQK 229
 SE+R + + +++ V+ ++S E TP
 Sbjct: 323 ---SEERAKDENEMLNQVRAAALSA-----ERTP----- 348

 Query: 230 SAKVYVILEKKHSRAATGILK--LLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDF 287
 + ++V I+ +K R GIL+ L+ D N +F P+D ++PRI + +
 Sbjct: 349 TGRIVGIVRRKW-RQYCGILQPSLIEDTNRH-----IFVPADRKIPIRIRIETRQAAM-- 399

 Query: 288 MTRPKDFANTLFICRIIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSS 347
 N I I W + + G +SLG G++ E E IL E+ V FS
 Sbjct: 400 -----LQNQRIIIVTIDTWPRNSRYPHGFVRSLGPLGDMATENEVILLEHDVPHCKFSD 453

 Query: 348 EVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARLDALACRRLTDGTFEVGVH 407
 EVL LP+ +PWTI ++ KR DLR I ++DP D+DDAL CR L +G EVGVH
 Sbjct: 454 EVLSFLPK-MPWTITDEDYSKRVDLRDLYICSVDPGCTDIDDAHCRELPGNLEVGVH 512

 Query: 408 IADVSYFPEGSSLDKVAERA-TSVYLVQKVVPMPLPRLLCIELCSLNPMTDKLTFSVIW 466
 IADVS+F+ G + T+VYLV K + M+P LL LCSL ++ FS +W
 Sbjct: 513 IADVSHFIRPGKRTGHGGSGPGETTVYLVGKRIDMVPPELLSSNLCSLVGGVERFAFSCVW 572

 Query: 467 KLTPEGKILEEWFGRTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXHSVEEVHQA 526
 ++ E +L + F ++I+S ++Y+ AQ++I++ E+ ++
 Sbjct: 573 EVDNEANVLSKRFHKSVIKSKRAMTYEEAQNIIDDATQQ-----NEIAKS 617

 Query: 527 VLNLHSIAKQLRRQRFDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFML 586
 + NL+ +AK L+++R +GAL L ++ F +D ET P + + R++N +VEEFMLL
 Sbjct: 618 LRNLNRLAKILKRRMDNGALVLASPEIRFQVDSETHEPLEVEVKQMRETNSMVEEFML 677

 Query: 587 ANMAVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKSLSKTF 646
 AN+ VA I F E A+LRRHP P LV+ G +D++S L+ SL K
 Sbjct: 678 ANITVAEHIATEFSECAVLRRHPRPPPTNFPLVKSARYQGFQVDINSGLELHSLDKCV 737

 Query: 647 -GDDKYSLARKEVLTNMYSRPMQMALYFCGMLQDQEQRHYALNVPLYTHFTSPIRRA 705
 D+ Y +LT +R M A+YF SG LQ +E+F HY L P+YTHFTSPIRRA++
 Sbjct: 738 KADNPYFNTMIRILT---TRCMMQAVYFISGSLQ-KEEFFHYGLAAPIYTHFTSPIRYS 793

 Query: 706 DVIVHRLLAALG---YSEQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVLVK 761
 D++VHRLLA++G Y++ D + + ++ + N R ++ S+ L + +
 Sbjct: 794 DIMVHRLLAASIGADSTYAQLLDRKSN--EELCHNLNYRHKAQYAGRASVALNTHLFFR 851

 Query: 762 ESGPLESEAMVMGVLNQAFDVLVLRFGVQKRIYCNALALRSYSFQKVGGKPELTLVWEPD 821
 + E V+ V A VL+ ++G++ +Y + ++V K E+ + +
 Sbjct: 852 GKEE-DEEGYVLFVRKNALQVLIPKYGLEGTLYLKSDKGKDGVERV--KSEIVFTFNEE 908

 Query: 822 DLEEPTQQVITIFSLVDVVLQAEATALKYSAILKR 857
 D + V F V V L +++ +++ ++ R
 Sbjct: 909 DHTQRCGDVVFHSFDPVTVRLSLDSSNVQHEKLIFR 944

>gi|5262619|emb|CAB45749.1| hypothetical protein [Homo sapiens]
Length = 632

Score = 334 bits (856), Expect = 4e-90
Identities = 226/644 (35%), Positives = 335/644 (52%), Gaps = 65/644 (10%)

Query: 222 LSEKSLQSAKVVYILEKKHSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLK 281
+SEK L+ + +VV I+ K++ R G+L . K S + LF+P+D R+PRI + +
Sbjct: 8 VSEKMLKPTGRVVGII-KRNWRPYCGMLSKSDIKES---RRHLFTPADKRIPRIRIETR 62

Query: 282 DCPQDFMTRPKDFANTLFICRII---DWKEDCNFALGQLAKSLGQAGEIEPETEGILTE 337
A+TL RII W + + G + +LG GE E ETE +L E
Sbjct: 63 Q-----ASTLEGRRIIIVAIIDGWPRNSRYPNGHFVRNLGDVGEKETETEVLLLE 110

Query: 338 YGVDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARLDLACRRL 397
+ V FS VL LP+ +PW+I ++ R DLR CI ++DP D+DDAL CR L
Sbjct: 111 HDVPHQPFSSQAVLSFLPK-MPWSITEKDMKNREDLRHLCICSVDPDGCTDIDDALHCREL 169

Query: 398 TDGTFEVGVHIADVSYFVPEGSSLDKVAAERATSVYLVQKVVPMLPRLCEELCSLNPM 457
+G EVGVHIADV+F+ G++LD+ +A R T+VYL +K + M+P LL LCSL
Sbjct: 170 ENGNLEVGVHIADVSHFIRPGNALDQESARRGTTVYLCEKRIDMVPELLSSNLCSLKCDV 229

Query: 458 DKLTFSVIWKLTPEGKILEEWFGRTIIRSCTKLSYDHQAQSMIENXXXXXXXXXXXXXX 517
D+L FS IW++ +IL+ F +++I S L+Y AQ I++
Sbjct: 230 DRLAFSCIWEMNHNAEILKTAKFTKSVINSKASLTYAFAQLRIDSANMN----- 277

Query: 518 HSVEEVHQAVLNLSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSN 577
+++ ++ L+ +AK L+++R GAL L ++ F +D ET P E R++N
Sbjct: 278 ---DDITTSRGLNKLAKILKKRRIEKGALTSSPEVRFHMDSETHDPIDLQTKELRETN 334

Query: 578 KLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGA 637
+VEEFMLLAN++VA KI F E ALLR+HP P LV+ L + +A +
Sbjct: 335 SMVEEFMLLANISVAKKIHEEFSEHALLRKHPAPPSNYEILVKAARSRNLEIKTDTAKS 394

Query: 638 LNKSLTKTFGDDKYSLARKEVLTNMYSRPMQMALYFCGMLQDQEQRHYALNVPLYTHF 697
L +SL + L + +R M A+YFCGSM D F HY L P+YTHF
Sbjct: 395 LAESLDQAESPTFPYL--NTLLRILATRCMMQAVYFCGMDND---FHHYGLASPIYTHF 449

Query: 698 TSPIIRRADVIVHRLAALG---YSEQPDVEPDQLQKQADHC---NDRRMASKRVQEL 750
TSPIIRR+ADVIVHRLA A+G Y E D K AD C N R ++ Q
Sbjct: 450 TSPPIRRYADVIVHRLAVALGADCTYPELTDK----HKLADICKNLNFRHKMAQYQAQRA 504

Query: 751 SIGLFFAVLVKESGPLLESEAMVMGVLNQAFDVLVLRFGVQKRIYCNALALRSYSFQKVGK 810
S+ + K G + EA ++ V A VL+ ++G++ + F +
Sbjct: 505 SVAFHTQLFFKSKKGIVSEEAYILFVRKNAIVVLI PKYGLETV-----FFEEKD 553

Query: 811 KPELTLVWEPDDLEEEPTQQVITIFSLVDVVLQAEATALKYSAI 854
KP L+++ + + V +F V V + +++ L++ I
Sbjct: 554 KPNPQLIYDDEIPSILKIEDTVFHVFDKVKVKIMLDSSNLQHQKI 597

>gi|27703387|ref|XP_224449.1| similar to mitotic control protein dis3 homolog [Homo sapiens]
[Rattus norvegicus]
Length = 1034

Score = 330 bits (846), Expect = 7e-89
Identities = 233/679 (34%), Positives = 343/679 (50%), Gaps = 69/679 (10%)

Query: 192 SISTPDRGKEDSSTPVMKDENTPIPIPQDTRGLSEKSLQSAKVVYILEKKHSRAATGILKL 251
S+ D G+ + V KDE + T +SEK L+ + +VV I+ K++ R G+L
Sbjct: 374 SVVLHDEGQNEDD--VEKDEERELLKT-AVSEKMLRPTGRVVGII-KRNWRPYCGMLSK 429

Query: 252 LADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFMTRPKDFANTLFICRIIDWKEDCN 311
K S + LF+P+D R+PRI + + + + I I W +
Sbjct: 430 SDIKES---RRHLFTPADKRIPRIRIETR-----QASALEGRRIIVAIIDGWPRNSR 477

Query: 312 FALGQLAKSLGQAGEIEPETEGILTEYGVDFSDSSEVLECLPQSLPWTIPPDEVGKRRD 371
+ G K+LG GE E ETE +L E+ V FS VL LP+ +PW+I +++ R D
Sbjct: 478 YPNGHFVKNLGDVGEKETETEVLLLEHDVPHQPFSQLSFLPK-MPWSITEEDMKNRED 536

Query: 372 LRKDCIFTIDPSTARLDALACRRLTDGTFEVGVHIADVSYFPEGSSLKDVAERATS 431
LR C+ ++DP D+DDAL CR L++G EVGVHIADVS+F+ G++LD+ +A R T+
Sbjct: 537 LRHLCVCSVDPGCTDIDDLHCRELSNGNLEVGVHIADVSHFIRPGNALDQESARRGTT 596

Query: 432 VYLVQKVVPMLPRLLCEELCSLNPMTDKL-----TFSVIWKLTPEGKILEEWFGR 482
VYL +K + M+P LL LCSL D+ F IW++ +IL+ F ++
Sbjct: 597 VYLCEKRIDMVPELLSSNLCSLRNSVDRYFCIVFDKXWHFPXIWE MNHNAEILKTRFTKS 656

Query: 483 IIRSCTKLSYDHAQSMIENXXXXXXXXXXXXHSVEEVHQAVLNLSIAKQLRRQRF 542
+I S L+Y AQ I++ +++ ++ L+ +AK L+R R
Sbjct: 657 VINSKASLTYAEAQMRIDSAA MN-----DDITTSLRGLNKLAKILKRGRI 701

Query: 543 VDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQ 602
GAL L ++ F +D ET P E R++N +VEEFMLLAN++VA KI F E
Sbjct: 702 EKGALTLSPEIRFHMDSETHDPIDLQTKELETRNSMVEEFMLLANISVAKKIHEEFSEH 761

Query: 603 ALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKS LT KTFGDDKYSLARKEVLTNM 662
ALLR+HP P LV+ L + +A +L SL + D L +L +
Sbjct: 762 ALLRKHPAPPPSNYEVLVKAASKNLEIRTDATKSLADSLDRAECPDFPYL--NTLLRIL 819

Query: 663 YSRPMQM ALYFCSGMLQDQEQRHYALNVPLYHTFTSPIRFAD VIVHRL LAAALG--- 718
+R M A+YFC SGM D F HY L P+YTHFTSPIRR+AD+IVHRL L A+G
Sbjct: 820 ATRCMMQAVYFCSGMDSD---FHHYGLASPIYHTFTSPI RRYADIIVHRL LAVAIGADCT 876

Query: 719 YSEQPDVEPDTLQKQADHC---NDRRMASKRVQELSIGLFFAVLVKESGPLESEAMVMGV 775
Y E D K +D C N R ++ Q S+ + K G + EA ++ V
Sbjct: 877 YPELTDK----HKLSDICKNLNFRHKMAQYAQRASVAFHTQLFFKSKGIVSEEAYILFV 931

Query: 776 LNQAFDVLVLRFGVQKRIYCNALALRSYSFQKVGKKPELT LVWEPDDLEEPTQQVITIF 835
A VL+ ++G++ ++ +K KP LT E L E T V +F
Sbjct: 932 RKNAIVVLIPKYGLETVFFE-----EKDKPKPRLTYDDEIPSLRIEGT--VFHV F 980

Query: 836 SLVDVVLQAEATALKYSAI 854
V V + +++ L++ I
Sbjct: 981 DKVKVKITLDSSNLQHQKI 999

Score = 51.6 bits (122), Expect = 5e-05
Identities = 30/99 (30%), Positives = 54/99 (54%), Gaps = 5/99 (5%)

Query: 49 IFETYMSKEDVSEGLKRGTLIQGVLRINPKKFHEAFI---PSPDGDRDIFIDGVVAR NRA 105
IF ++ + +G+K G+ +QG R + + + EA + + + +I I G+ NRA
Sbjct: 294 IFSEHLPLSKLQQGIKSGSYLQGTFRASRENYLEATVWIHGDK EDEKEILIQGLKHLNRA 353

Query: 106 LNGDLVVVKLLPEDQWKAVKPESNDKEIEATYEADIP EEE 144
++ D+V V+LLP+ QW V P S E E D+ ++
Sbjct: 354 IHEDIVAVELLPKSQW--VAPSSVVLHDEGQNEDDVEKD 390

>gi|19923416|ref|NP_055768.2| mitotic control protein dis3 homolog [Homo sapiens]
gi|17225572|gb|AAL37479.1|AF330044_1 KIAA1008 protein [Homo sapiens]
Length = 958

Score = 330 bits (845), Expect = 7e-89
Identities = 229/674 (33%), Positives = 344/674 (51%), Gaps = 68/674 (10%)

Query: 192 SISTPDRGKEDSSTPVMKDENTPIPQDTRGLSEKSLQSAKVVYILEKKHSRAATGILKL 251
S+ D G+ + ++ + +SEK L+ + +VV I+ K++ R G+L
Sbjct: 307 SVVLHDEGQNEEDVEKEEETERMLKT---AVSEKMLKPTGRVVGII-KRNWRPYCGMLSK 362

Query: 252 LADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFMTRPKDFANTLFICRII----DWK 307
K S + LF+P+D R+PRI + + A+TL RII W
Sbjct: 363 SDIKES----RRHLFTPADKRIPRIETRQ-----ASTLEGRRIIVAIIDGWP 406

Query: 308 EDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDSSEVLECLPQSLPWTIPPDEVG 367
+ + G ++LG GE E ETE +L E+ V FS VL LP+ +PW+I ++
Sbjct: 407 RNSRYPNGHFVRNLGDVGEKETETEVLLLEHDVPHQFSQAVLSFLPK-MPWSITEKDMK 465

Query: 368 KRRDLRKDCIFTIDPSTARLDALACRRLTDGTFEVGVHIADVSYFVPEGSSLKDVAEE 427
R DLR CI ++DP D+DDAL CR L +G EVGVHIADVS+F+ G++LD+ +A
Sbjct: 466 NREDLRHLCICSVDPDGCTDIDDALHCRELENGNLEVGVHIADVSHFIRPGNALDQESAR 525

Query: 428 RATSVYLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPEGKILEEWFGRTIIRSC 487
R T+VYL +K + M+P LL LCSL D+L FS IW++ +IL+ F +++I S
Sbjct: 526 RGTTVYLCEKRIDMVPELLSSNLCSLKCDVDRLAFSCIWEMNHNAEILKTFTKSVINSK 585

Query: 488 TKLSYDHAQSMIENXXXXXXXXXXXXHSVEEVHQAVLNHSIAKQLRRQRFVDGAL 547
L+Y AQ I++ +++ ++ L+ +AK L+++R GAL
Sbjct: 586 ASLYTAEQLRIDSANMN-----DDITTSRGLNKAKILKKRRIEKGAL 630

Query: 548 RLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRR 607
L ++ F +D ET P E R++N +VEEFMLLAN++VA KI F E ALLR+
Sbjct: 631 TLSSPEVRFHMDSETHDPIDLQTKELRETNSMVEEFMLLANISVAKKIHEEFSEHALLRK 690

Query: 608 HPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKS LT KTFGDDKYSLARKEVLTNMYSRPM 667
HP P LV+ L + +A +L +SL + L +L + +R M
Sbjct: 691 HPAPPPSNYEILVKAARSRNLEIKDTAKSLAESLDQAESPTFPYL--NTLLRILATRCM 748

Query: 668 QMALYFCSGMLQDQEQRHYALNVPLYTHFTSPIRFADVVHRLAALG---YSEQP 723
A+YFCSGM D F HY L P+YTHFTSPIRR+ADVIVHRLLA A+G Y E
Sbjct: 749 MQAVYFCGMDND---FHHYGLASPIYTHFTSPIRYADVIVHRLLAVAIGADCTYPELT 805

Query: 724 DVEPDTLQKQADHC---NDRRMASKRVQELSIGLFFAVLVKE SGPLESEAMVMGVLNQAF 780
D K AD C N R ++ Q S+ + K G + EA ++ V A
Sbjct: 806 DK-----HKLADICKNLNFRHKMAQYAQRASVAFHTQLFFKSKGIVSEEAYILFVRKNAI 860

Query: 781 DVLVLRFGVQKRIYCNALALRSYSFQKVGKKPELTLVWEPPDDLEEPTQQVITIFSLVDV 840
VL+ ++G++ + F + KP L+++ + + V +F V V
Sbjct: 861 VVLIIPKYGLETV-----FFEEKDKPNPQLIYDDEIPSLKIEDTVFHVFDFKV 909

Query: 841 VLQAEATAALKYSAI 854
+ + + L++ I
Sbjct: 910 KIMLDSSNLQHQKI 923

Score = 50.1 bits (118), Expect = 2e-04
Identities = 27/83 (32%), Positives = 48/83 (57%), Gaps = 5/83 (6%)

Query: 49 IFETYMSKEDVSEGLKRGTLIQGVLRINPKKFHEAFI---PSPDGDRDIFIDGVVARNRA 105
IF ++ + +G+K GT +QG R + + + EA + + + +I + G+ NRA
Sbjct: 227 IFSEHLPLSKLQQGIKSGTYLQGTFRASRENYLEATVWIHGDSSEENKEIILQGLKHLNRA 286

Query: 106 LNGDLVVVKLLPEDQWKAVKPES 128
++ D+V V+LLP+ QW V P S
Sbjct: 287 VHEDIVAVELLPKSQW--VAPSS 307

gi|6324552|ref|NP_014621.1| Possible component of RCC1-Ran pathway; Dis3p [Saccharomyces cerevisiae]

gi|2500547|sp|Q08162|RR44_YEAST Exosome complex exonuclease RRP44, Ribosomal RNA processing protein 44) (Protein DIS3)

gi|2131990|pir||S66704 hypothetical protein YOL021c - yeast (Saccharomyces cerevisiae)

gi|1419801|emb|CAA99021.1| ORF YOL021c [Saccharomyces cerevisiae]

gi|1754617|dbj|BAA11176.1| DIS3 protein [Saccharomyces cerevisiae]
Length = 1001

Score = 321 bits (823), Expect = 3e-86
Identities = 253/761 (33%), Positives = 364/761 (47%), Gaps = 99/761 (13%)

Query: 50 FETYMSKEDVSEGLKRGTЛИQGVLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNGD 109
F Y S V GLK G L QG ++I+ F E + P + + I G NRA NGD
Sbjct: 255 FPEYYSTARVMGGLKNGVLYQGNIQISEYNFLEGSVSLPRFSKPVLIVGQKNLNRAFNGD 314

Query: 110 LVVVKLLPEDQWKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSGPDVIIEAQF 169
V+V+LLP+ +WKA D E H + + PD IEA
Sbjct: 315 QVIVELLPQSEWKAPSSIVLDSE-----HFDVNDN-----PD--IEAG- 350

Query: 170 DDSDSED RHGNTSGLVDGVKKLSISTPDRGKEDSSTPVMDENTPIPIPQDTRGLSEKSLQK 229
DD D+ + NT+ + D ++L + KD I Q + K +Q
Sbjct: 351 DDDDNNESSNTTVisDKQRRL-----LAKD-AMIAQRS----KKIQP 388

Query: 230 SAKVYYILEKKHSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLKD-CPQDFM 288
+AKVYYI +++ R G LA + D P + +V L D C
Sbjct: 389 TAKVYYI-QRRSWRQYVG---QLAPSSVD-----PQSSSTQNVFVILMDKCLPKVR 435

Query: 289 TRPKDFANTL---FICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDF 345
R + A L + I W + LG + LG + ETE +L E+ V++ F
Sbjct: 436 IRTRRAEELLDKRIVISIDSWPTTHKYPLGHFVRDLGTIESAQAEATEALLLEHDVEYRPF 495

Query: 346 SSEVLECLP-QSLPWTIP----PDEVG-----KRRDLRKDCIFTIDPSTARDDALA 393
S +VLECLP + W P P+ V KR+DLR I +IDP D+DDAL
Sbjct: 496 SKKVLECLPAEGHDWKAPTKLDDPEAVSKDPLLTKRKDLRDKLICSIDPPGCVDIDDALH 555

Query: 394 CRR LTDGT FEVGVHIADVS YFVPEGSSL DKVAAERAT SVYL VQK VV PM LP RL CEELCSL 453
++L +G +EVGVHIADV++FV G++LD A R TSVYLV K + MLP LL +LC SL
Sbjct: 556 AKKL PNGNWEVGVHIADV THFVKPGT ALDAEGAARGT SVYLV DKRIDMLPM LLG TD LCSL 615

Query: 454 NPMTDKLTFSVIWKLTP EGKILEEWFGRTIIRSCTKLSYDHAQSMIENXXXXXXXXXX 513
P D+ FSVIW+L I+ F + + + IRS SY+ AQ I++
Sbjct: 616 KPYVDRFAFSVIWELDDSANIVNVNFMKS VIRS REAFSYEQAQLRIDDKTQN----- 667

Query: 514 XXXXHSVEEVHQAVLN LHSIAKQLRRQRFVDGALR LDQLKLAFTLDHETGLPQGCHIYEY 573
+E+ + L ++ +L++ +R GAL L ++ +D ET P I +
Sbjct: 668 -----DELT MGR ALLKL SVKL QKR LEAG ALN LASPEV KVHM DSET SDP NEVEIKKL 720

Query: 574 RDS NKLVEEFM LLANMAVAHK IFR TFPEQ ALL RRH PPP QT KMLSDLV EFCD -QM GLP MDV 632
+N LVEEFM LLAN++VA KI+ FP+ A+LRRH P + L E + + + +
Sbjct: 721 LAT NSLVEEFM LLANISVARKIYDAFP QT AML RRH APP STN FEIL NEM LNTR KNMS ISL 780

Query: 633 SSAGALNKS LT KTFG -DDK YSLARKEV LTN MYSRPM QM ALYFC SGML QDQE QFRHY AL NV 691
S+ AL SL + +D Y ++ M +R M A YF SG FRHY L V
Sbjct: 781 ESS KALADSL DRC VDP ED PYF ---NTL VRIM STR CMMA QYFY SGAYS -YPD FRHY GLAV 836

Query: 692 PLYTHFTSPIR RFAD VIVH RLLA A ALG YSEQ P DVEPD --TLQ KQADHC ND RR MASK RVQE 749
+YTHFTSPIR + DV+ HR LA A+GY D + + N + ++
Sbjct: 837 DIYTHFTSPIR YCDV VA HR QL AIG YEP SLTHR DKN KMD M ICRN IN R KHR NAQ FAGR 896

Query: 750 LSIGLFFAVLVK ESG PLE SEAM VMG VL NQAF DV L VL RFG VQ 790
SI + + + + E+ V+ V N VLV + FGV+
Sbjct: 897 ASIE YYVGQ VMR NN ESTET -GYVI KV FN NGI VV L VP KFG VE 936

>gi|21297331|gb|EAA09476.1| ebiP3704 [Anopheles gambiae str. PEST]
Length = 965

Score = 313 bits (803), Expect = 6e-84
Identities = 228/691 (32%), Positives = 352/691 (50%), Gaps = 62/691 (8%)

Query: 180 NTSG LVDGVKKLSISTPDRGKEDSSTPVMDENTPI----PQDTRGLSEKSLQK-SAKV 233

N + VDG P+ + S V+ DE T P T + ++ ++ +AKV
Sbjct: 280 NLNRAVDGDTVAIEMLPSEWKA PSDVVLVDEQTDPGDMVEPDPTFSVKPQAEREPTAKV 339

Query: 234 VYILEKKHSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFMTRPKD 293
V I+++K R GIL + S +F P++ ++PRI + +
Sbjct: 340 VGIIKRKW-RQYCGILLPSHIQGS---TRHIFVPAERKIPRIRIETRQ----- 383

Query: 294 FANTLFICRII---DWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDSSEV 349
A TL RII W + G ++LG G E E E IL E+ V S FS +V
Sbjct: 384 -AATLLSQRIIVAIIDQWPRHSRYPQGHFVRALGPIGSKETENEVILLEHDVPHSRFSEDV 442

Query: 350 LECLPQSLPWTTIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTDGTFEVGVHIA 409
L CLP+ LPWTI ++ +R DLR + ++DP D+DDAL RRL +G EVGVHIA
Sbjct: 443 LACLPE-LPWTITAADLQRRVDLRDITVCSVDPGCTDIDDALHARRLPNGNIEVGVHIA 501

Query: 410 DVSYFVPEGSSLDKVAERATS VYLVQKVVPMLPRLLC EELCSLNPM TDKLTF SVIWKLT 469
DV +F+ G++LD+ AA RAT+VYLV K + M+P LL LCSL ++ FS IW+L
Sbjct: 502 DVGHFIRPGTALDREAASRATTVYLVDKRIDMVPGLLSSNLCSLRGGEERFAFSCIWLD 561

Query: 470 PEGKILEEWFGR TIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXHSVEEVHQAVLN 529
E I + +++I+S + L+Y+ AQ +I++ +V ++
Sbjct: 562 DEANIRNTRYHKSVIKSKSALT YEEAQIIIDD-----AKQTNDVATSLRL 606

Query: 530 LHSIAKQLRRQRFDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANM 589
L+ +AK L+++R GAL L ++ F +D ET P + ++N +VEEFMLLAN+
Sbjct: 607 LNRLAKILKKRTEKGALV LASPEIRFQVDSETHPIDVKAKQLLETNSMVEEFMLLANV 666

Query: 590 AVAHKIFRTFPEQALLRRHPPPQT KMLSDLVEFC DQMGLPM DVSSAGALNKS LT KTFGDD 649
+VA KI + FPE A+LRRHP P LV+ + G + +S L SL K D
Sbjct: 667 SVAEKIEQEFP ECAMLRRHPCPPQ ANYEPLV KAAEHQGFEIL TSGKELATSLDKAVKPD 726

Query: 650 KYSLARKEVLT NMSRPQM ALYFC SGM LQDQE QFRHYALNVPLYTHFTSPIR FADVIV 709
+L + +R M A+YF SG +Q ++F HY L P+YTHFTSPIR +AD+IV
Sbjct: 727 NPYF--NTMLRILATRCMMQAVYFISGT VQ-RDEF HYGLA APIYTHFTSPIR YADIIV 783

Query: 710 HRLLAA ALGYSEQPDVEPDTLQKQADH--CND---RRMASKRVQELSIGLFFAVLVKESG 764
HRLLAA +G P+ L K+ + CN+ R ++ S+ L + ++
Sbjct: 784 HRLLAACIGADS---TYPE LDKKVNSNLCNNLNYRN RMAQYAGRASVALHTHLFFRKRS 840

Query: 765 PLESEAMVMGVLNQAFDVLVLRFGVQKR IYCNA LALRSYSFQKVGKKPELTLVWE PDDLE 824
+ +A ++ + A +LV ++G + IY R+ K G + V++ +
Sbjct: 841 E-DEQAYILFIRKNALQILV PKYGFEGTIYVTG---RNNEEIKTGVR---FVYDEEQQT 892

Query: 825 EEPTQQVITIFS LVDVVLQAEATALKY SAIL 855
+ Q V F V V L ++T +++ ++
Sbjct: 893 QR CGQVVFRAFDPVIVRLSLDSTNVQHEKLV 923

Score = 53.1 bits (126), Expect = 2e-05
Identities = 23/75 (30%), Positives = 46/75 (61%)

Query: 49 IFETYMSKEDVSEGLKRGTLI QGVLRINPKKFHEAFIPS PGDRDIF IDGVVARNRALNG 108
+F +++++ + EG+K G L+QG + + + E ++ ++ + I G + NRA++G
Sbjct: 228 LFPSHLTMLQIHEGIKGGKLMQGGFLASRE NYLEGYVR VEGIEKAVL IQGRMN LNRAVDG 287

Query: 109 DLVVVKLLPEDQWKA 123
D V +++LPE +WKA
Sbjct: 288 DTVAIEMLPSEWKA 302

>gi|14250908|emb|CAC39259.1| Rrp44p homologue [Trypanosoma brucei]
Length = 972

Score = 313 bits (801), Expect = 1e-83
Identities = 187/536 (34%), Positives = 289/536 (53%), Gaps = 35/536 (6%)

Query: 265 LFSPSDHRVPRIYVPLKDCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQA 324
LF P D+R+PRI + D + I DW E +F +G + LG
Sbjct: 396 LFQPKDNRIPRIRIT-----TAHLGDLKDKRLSVIIDDWGEHSSFPVGHYVEVLGTI 447

Query: 325 GEIEPETEGILTEYGVDIFSDSSEVLECLPQLPWTIPPDEVGKRRDLRKDCIFTIDPST 384
G+ + E + IL E + DFS V +CLP+ W + +E+G R DLR C+ ++DP
Sbjct: 448 GDKDTEAKVILLENDIPHDFSEAVYDCLPKG-EWNVTTEEELGNRLDLCVSVDPLG 506

Query: 385 ARDLDDALACRRLTDGTFEVGVHIADVSYFPEGSSLKDVAERATSVYLVQKVVPMLPR 444
RD+DDAL CRR+ EVGVHIADV++F+ EG++D+ AA+R+TSVYLV + + MLP+
Sbjct: 507 CRDIDDALHCRRVNGNHLEVGVHIADVTFLKEGTAMDEEAKRSTSVDLDRINMLPQ 566

Query: 445 LLCEELCSLNPMTDKLTFSVIWKLTPEGKILEEWFGRTIIRSCTKLSYDHAQSMIENXXX 504
LL E LCS+ D+ FS++W+ ++ E+FG+T+IRS L Y AQ MI++
Sbjct: 567 LLTENLCSIVADEDRYAFSIMWEFDENYSVVREFFGKTVIRSRAALYYGDAQRMIIDDPED 626

Query: 505 XXXXXXXXXXXXXHSVEEVHQAVLNHSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGL 564
E ++ L +++ R++R DGAL L + F +D++
Sbjct: 627 E-----SEAAVSLRYLMQLSRHFRKRREKGALFLCSQEKFVVDNDHVN 671

Query: 565 PQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFC- 623
P Y+ DSN ++EE+ML AN A A +++ +FP LLRRH P L E
Sbjct: 672 PTDMQAYQTDFDSNSMIEEWMOLFANAAAARRVYASFPRWTLLRRHQAPAENAFDTLNEAIR 731

Query: 624 DQMGLPMDVSSAGALNKS LT KTFGDDKYSLARKEVLTNMYSRPMQM ALYFCGMLQDQE 683
++G+ +D +++ ALN+SL K R ++ + +R ++ A YF S + +++
Sbjct: 732 RKIGVKLDDTTSLALNESLEKCVDPSDPYFNR--LIRTLVTRCLRQAQYFSSSEVS-KDE 788

Query: 684 FRHYALNVPLYTHFTSPIRRFADVIVHRLAALGYSEQPDVEPDTLQKQ--ADHCNDRR 741
F H+ L +P+YTHFTSPIRR+ADVIVHRLAALG + + + + + A + N R
Sbjct: 789 FHHGLAMPIYTHFTSPIRRYADVIVHRLAALGIMDVSEAHMVSVKMEALASNLNYRH 848

Query: 742 MASKRV---QELSIGLFFAVLVKESGPLEEAMVMGVLNQAFDVLVLRFGVQKRI 793
++R Q L G + + P E +V F VLV ++G + +I
Sbjct: 849 EQAQRAGRDSQNLFYLRNFANQEIPSEDGYVVKLSETHVF-VLVPKYGQEGKI 903

Score = 40.0 bits (92), Expect = 0.17
Identities = 26/115 (22%), Positives = 52/115 (45%), Gaps = 9/115 (7%)

Query: 49 IFETYMSKEDVSEGLKRGTLIQGVLRINPKKFHEAFIPS P DGD-----RDIFIDGVVAR 102
+F + + + + G++ GT + +G LR++ F G + + G
Sbjct: 235 LFSPHLAESALDLGVQNGTYLRGKLRVSETN---CFFGEIRGQWKGHNFERVLLPGRTNL 291

Query: 103 NRALNGDLVVVKLLPEDQWKAVKPESNDKEIEATYEADIP EEGCGHPLQQSRKG 157
NRA++GD+V V+LLP W+ ++ +E+ T E G + + +G
Sbjct: 292 NRAIHGDIVTVELLPVASWRPLRGAKPTEEMNDTGAGGDDHENSGREGIGEESEG 346

>gi|19113445|ref|NP_596653.1| mitotic control protein dis3
[Schizosaccharomyces pombe]
gi|585053|sp|P37202|DIS3_SCHPO Mitotic control protein dis3
gi|283075|pir|A41944 mitotic control protein dis3+ - fission yeast
(Schizosaccharomyces
pombe)
gi|173381|gb|AAA35302.1| mitotic control protein
gi|3650393|emb|CAA21102.1| mitotic control protein dis3
[Schizosaccharomyces pombe]
Length = 970

Score = 301 bits (770), Expect = 4e-80
Identities = 202/594 (34%), Positives = 301/594 (50%), Gaps = 43/594 (7%)

Query: 218 DTRGLSEKSLQKSAKVVYILEKKHSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIY 277
D + + + + +AKVV IL++ + + + + L +P D RVP+I
Sbjct: 348 DLELITKRNAHPTAKVVGILKRNWRPYVGHVDNATIAQSKGGSQQTVLTPMDRRVPKIR 407

Query: 278 VPLKDCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTE 337
+ P+ R + I W + G + LG+ E ETE +L E
Sbjct: 408 FRTRQAPRLVGRR-----IVVAIDLWDASSRYPEGHFVRDLGEMETKEAETEALLLE 459

Query: 338 YGVDFSDSSEVLECLPQS-LPWTIPPDEV---GKRRDLRKDCIFTIDPSTARLDLDDAL 392
Y V F VL+CLP+ W +P D+ R+D R I +IDP +D+DDAL
Sbjct: 460 YDVQHHRPFPAVLDCLPPEEGHNWKVPADKTHPLWKNRKDFRDKLICSIDPPGCQDIDDAL 519

Query: 393 ACRRLTDTGTFEVGVHIADVSYFVPEGSSLDKVAERATSVYLVQKVVPMLPRLLCEELCS 452
L +G +EVGVHIADV++FV +S+D AA R T+VYLV K + MLP LL +LCS
Sbjct: 520 HACVLPNGNYEVGVHIADVTHFVKPNTSMDEAASRGTTVYLVDKRIDMLPMILLGTDLCS 579

Query: 453 LNPMTDKLTFSVIWKLTPEGKILEEWFGRTIIRSCTKLSYDHAQSMIENXXXXXXXXX 512
L P ++ FS IW++ I++ F +++I S SY AQ+ I++
Sbjct: 580 LRPyVERFAFSCIWEMDENANIIKVHFTKSVIASKEAFSYADAQARIDDQKMQ----- 632

Query: 513 XXXXXHSVEEVHQAVLNLSIAKQLRRQRFDGALRLDQLKLAFTLDHETGLPQGCHIYE 572
+ + Q + L ++K L+++R +GAL L ++ D+ET P I +
Sbjct: 633 -----DPLTQGMRVLLKLSKILKQKRMDEGALNLASPEVRIQTDNETSDPMVDEIKQ 684

Query: 573 YRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRH-PPPQTKM--LSDLVEFCDQMGLP 629
++N LVEEFMLLAN++VA KI+ FP+ A+LRRH PP T L D++ C M L
Sbjct: 685 LLETNSLVEEFMLLANISVAQKIYDAFPQTAVLRRHAAPPLTNFDLQDILRVCKGMHLK 744

Query: 630 MDVSSAGALNKSLLKTFGD--DKYSLARKEVLTNMYSRPMQMALYFCGMLQDQEQRHY 687
D S KSL K+ + D +L + +R M A YFCSG + FRHY
Sbjct: 745 CDT-----KSLAKSLDECVDPKEPYFNTLLRILTRCMLSAEYFCSGTFAPPD-FRH 797

Query: 688 ALNVPLYHTFTSPIRRFADVIVHRLLAAALGYSE-QPDV-EPDTLQKQADHCNDRRMASK 745
L P+YTHFTSPIRR+ADV+ HR LAAA+ Y P + + L + + N R ++
Sbjct: 798 GLASPIYHTFTSPIRRYADVLahrqlaaaIdyETINPSLSDKSRLIEICNGINYRHRMAQ 857

Query: 746 RVQELSIGLFFAVLVKESGPLESEAMVMGVLNQAFDVLVLRFGVQKRIYCNALA 799
SI + +K G E +A V+ V F V + RFG++ +Y +L+
Sbjct: 858 MAGRASIEYYVGQALK-GGVAEEDAYVIKFNGFVVFIARFGLEGIVYTKSLS 910

Score = 49.7 bits (117), Expect = 2e-04
Identities = 23/84 (27%), Positives = 46/84 (54%)

Query: 49 IFETYMSKEDVSEGLKRGTLIQGVLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNG 108
++E + S + +K G + +G++ I+ + E + P ++ + + G NRA+ G
Sbjct: 247 VYELHWSMSRLLACIKNGEVHKGLINISTYNYLEGSVVPGYNKPVLVSGRENLNRAVQG 306

Query: 109 DLVVVKLLPEDQWKAVKPESNDKE 132
D+V + +LP+DQWK E D +
Sbjct: 307 DIVCIQILPQDWKTEAEETADD 330

>gi|15021874|dbj|BAB62212.1| hypothetical protein [Macaca fascicularis]
Length = 249

Score = 291 bits (745), Expect = 3e-77
Identities = 156/247 (63%), Positives = 171/247 (69%), Gaps = 2/247 (0%)

Query: 1 MNHPDYKLNRLXXXXXXXXXXXXXXXXXXXXXIFETYMSKEDVS 60
M+HPDY++NLR D IFETYM KEDVS
Sbjct: 1 MSHPDYRMNLRPLGTPRGVSTVAGPHGIGASPGDKSKNKSTRGKKKSIFETYMFKEDVS 60

Query: 61 EGLKRGTLIQGVLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNGDLVVVKLLPEDQ 120
EGLKRGTLIQGVLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNGDLVVVKLLPE+Q
Sbjct: 61 EGLKRGTLIQGVLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNGDLVVVKLLPEEQ 120

Query: 121 WKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWS-GPDVIIEAQFDDSDSEDRHG 179
WK VKPE+NDKE EA YE+DIPEE CG H QQS K ++ PDVIIIEAQFD SDSED HG

Sbjct: 121 WKVVKPENNDKETEAAYESDIPEELCGRHLQQSLKSYNDSPDVIIEAQFDGSDSEDGHG 180

Query: 180 NTSG-LVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPQDTRGLSEKSLQKSAKVVYILE 238

T LVD VKKLS+ ++G+E PV KDE T I QDTR L EKSLQ+SAKV+

Sbjct: 181 ITQNVLVDDVKKLSVCVSEKGREHGDAPVTKDETTCISQDTRALPEKSLQRSAKVIAYRF 240

Query: 239 KKHSRAA 245

H + A

Sbjct: 241 SSHVQMA 247

>gi|19115966|ref|NP_588616.1| hypothetical protein MGC4562 [Homo sapiens]
gi|18314381|gb|AAH22089.1|AAH22089 Similar to mitotic control protein dis3
homolog [Homo sapiens]
Length = 971

Score = 284 bits (727), Expect = 4e-75

Identities = 190/586 (32%), Positives = 297/586 (50%), Gaps = 50/586 (8%)

Query: 265 LFSPSDHRVPRIYVPLKDCP--QDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLG 322

L +P D+R+P+I + + QDF + RI W+ + G + LG

Sbjct: 283 LVTPWDYRIPKIRISTQQAETLQDFRV-----VVRIDSWESTSVYPNGHFVRVLG 332

Query: 323 QAGEIEPETEGILTEYGVDFSDSSEVLECLPQSL---PWTIPPDEVGKRRDLRKD-CIF 378

+ G++E E IL E + FS + +P + PW + P+E KR+DLRK +F

Sbjct: 333 RIGDLEGEIATILVENSISVIPFSEAQMCEMPVNTPESPWVKSPEEEQKRKDLRKSHLVF 392

Query: 379 TIDPSTARLDALACRRLTDGTFEVGVHIADVSYFVPEGSSLKVAERATSVYLVQKV 438

+ IDP D+DD L+ R L +G E+GVHIADV++FV S +D A RAT+ YL +

Sbjct: 393 SIDPKGCEVDVDTLSVRTLNNGNLELGVHIADVTHFVAPNSYIDIEARTRATTYYLADRR 452

Query: 439 VPMLPRLLCEELCSLNPMTDKLTFSVIWKLPEG-KILEEWFGRTIIRSCTKLSYDHAQS 497

MLP +L +LCSL D+ S++W+L +I + W+GRTIIRS KL Y+ AQ

Sbjct: 453 YDMLPSVLSADLCSSLGGVDRYAVSIMWELDKASYEIKVWYGRTIIRSAYKLFYEAAQE 512

Query: 498 MIENXXXXXXXXXXXXXXHS---VEEVHQAVLNLSIAKQLRRQRFVDGALRLDQLK 553

+++ S +EE+ A+ L IA+ +R +R GAL L+ ++

Sbjct: 513 LLDGNLSVVDDIPEFKDLDEKSRAKLEELVWAIGKLTDIARHVRAKRDGCGALELEGVE 572

Query: 554 LAFTLD----HETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRH 608

+ LD H+ Q ++E V E M+LAN VA KI+ +FP QALLR+H

Sbjct: 573 VCVQLDDKKNIHDLIPKQPLEVHE-----TVAECMILANHWAKKIWESFPHQALLRQH 626

Query: 609 PPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKS LT KTFGDDKYSLARKEVLTNMYSRPMQ 668

PPP + S+L E G +D S L SL +D + +L +M ++ M

Sbjct: 627 PPPHQEFFSELRECAKAKGFFIDTRSNKTLADSLDN--ANDPHDPIVNRLLRSMATQAMS 684

Query: 669 MALYFCGMLQDQEQRHYALNVPLYTHFTSPIRFADIVVHRLLAALGYSEQPDVEPD 728

ALYF +G +E+F HY L+ YTHFTSPIRR++D++VHRL AA+ ++ +++ +

Sbjct: 685 NALYFSTGS -EEFHGYGLALDKYTHFTSPIRRYSDIVVHRLMAAISDKKMEIKGN 743

Query: 729 ----TLQKQADHCNDRRMASKRVQELSIGLFFAVLVKESGPL-----SEAMVMGVLNQ 778

L++ H N+R A++ Q+ S LF + K+ P S+ ++ +

Sbjct: 744 LFSNKDLEELCRHINNRNQAAQHSQKQSTELFQCMYFKDKDPATEERCISDGVIYSIRTN 803

Query: 779 AFDVLVLRFGVQKRIYCNALALRSYSFQKVGKKPELTLVWEPPDLE 824

+ + RFG++ Y L++ + P+ W+P L+

Sbjct: 804 GVLLFIPRGFIKGAAY----LKNKDGLVISCGPDSCSEWKPGSLQ 844

Score = 59.3 bits (142), Expect = 3e-07

Identities = 33/82 (40%), Positives = 51/82 (62%), Gaps = 8/82 (9%)

Query: 50 FETYMSKEDVSEGLKRGTLIQGVLRINPKKFH-EAFI-----PSPDGD--RDIFIDGVVA 101

+ ++ E + G+K G IQG+L +N + EAF+ S D D DI I G+ A

Sbjct: 142 YPEHLPLEVLEAGIKSGRYIQGILNVNKHRAQIEAFVRLQGASSKDSLVDILIHMKA 201

Query: 102 RNRALNGDLVVVKLLPEDQWKA 123
RNR+++GD+VVV+LLP+++WK
Sbjct: 202 RNRSIHGDVVVVELLPKNEWKG 223

>gi|18916779|dbj|BAB85541.1| KIAA1955 protein [Homo sapiens]
Length = 947

Score = 284 bits (726), Expect = 5e-75
Identities = 190/586 (32%), Positives = 297/586 (50%), Gaps = 50/586 (8%)

Query: 265 LFSPSDHRVPRIYVPLKDCP--QDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLG 322
L +P D+R+P+I + + QDF + RI W+ + G + LG
Sbjct: 259 LVTPWDYRIPKIRISTQQAETLQDFRV-----VVRIDSWESTSVYPNGHFVRVLG 308

Query: 323 QAGEIEPETEGILTEYGVDFSDFSSEVLECLPQLS---PWTIPPDEVGKRRDLRKD-CIF 378
+ G++E E IL E + FS + +P + PW + P+E KR+DLRK +F
Sbjct: 309 RIGDLEGEIATILVENSISVIPFSEAQMCEMPVNTPESPWKVSPEEEQKRKDLRKSHLVF 368

Query: 379 TIDPSTARLDALACRRLTDGTFEVGVIADVSYFPEGSSLKVAERATSVYLVQKV 438
+IDP D+DD L+ R L +G E+GVHIADV++FV S +D A RAT+ YL +
Sbjct: 369 SIDPKGCEVDVDDTLSVRTLNNGNLELGVHIADVTHFVAPNSYIDIEARTRATTYYLADRR 428

Query: 439 VPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPKG-KILEEWFGRTIIRSCTKLSYDHAQS 497
MLP +L +LCSL D+ S++W+L +I + W+GRTIIRS KL Y+ AQ
Sbjct: 429 YDMLPSVLSADLCSSLGGVDRYAVSIMWELDKASYEIKVWYGRTIIRSAYKLFYEAAQE 488

Query: 498 MIENXXXXXXXXXXXXXXHS---VEEVHQAVLNLSIAKQLRRQRFDGALRLDQLK 553
+++ S +EE+ A+ L IA+ +R +R GAL L+ ++
Sbjct: 489 LLDGNLSVVDDIPEFKDLDEKSRAKLEELVWAIGKLTDIRHVRAKRDGCGALELEGVE 548

Query: 554 LAFTLD----HETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRH 608
+ LD H+ Q ++E V E M+LAN VA KI+ +FP QALLR+H
Sbjct: 549 VCVQLDDKKNIHDLIPKQPLEVHE----TVAECMILANHWVAKKIWESFPHQALLRQH 602

Query: 609 PPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKS LT KTFGDDKYSLARKEVLTNMYSRPMQ 668
PPP + S+L E G +D S L SL +D + +L +M ++ M
Sbjct: 603 PPPHQEFFSELRECAKAKGFFIDTRSNKTLADSLDN--ANDPHDPIVNRLRSMATQAMS 660

Query: 669 MALYFCSGMLQDQEQRHYALNVPLYTHFTSPIRFADIVHRLAALGYSEQPDVEPD 728
ALYF +G +E+F HY L + YTHFTSPIRR++D++VHRL AA+ ++ +++ +
Sbjct: 661 NALYFSTGSAC-EEEFHGHGLALDKYTHFTSPIRRYSDIVVHRLLMAAISKDKKMEIKGN 719

Query: 729 ----TLQKQADHCNDRRMASKRVQELSIGLFFAVLVKESGPL-----SEAMVMGVLNQ 778
L++ H N+R A++ Q+ S LF + K+ P S+ ++ +
Sbjct: 720 LFSNKDLEELCRHINNRNQAAQHSQKQSTELFQCMYFKDKDPATEERCISDGVIYSIRTN 779

Query: 779 AFDVLVLRFGVQKRIYCNALALRSYSFQKVGKKPELTLWEPDDLE 824
+ + RFG++ Y L++ + P+ W+P L+
Sbjct: 780 GVLLFIPRGFIKGAAY----LKNKDGLVISCGPDSCSEWKPGSLQ 820

Score = 59.3 bits (142), Expect = 3e-07
Identities = 33/82 (40%), Positives = 51/82 (62%), Gaps = 8/82 (9%)

Query: 50 FETYMSKEDVSEGLKRGTLIQQVLRINPKKFH-EAFI----PSPDGD--RDIFIDGVVA 101
+ ++ E + G+K G IQG+L +N + EAF+ S D D DI I G+ A
Sbjct: 118 YPEHLPLEVLEAGIKSGRYIQGILNVNKHRAQIEAFVRLQGASSKDSLVDILIHGMKA 177

Query: 102 RNRALNGDLVVVKLLPEDQWKA 123
RNR+++GD+VVV+LLP+++WK
Sbjct: 178 RNRSIHGDVVVVELLPKNEWKG 199

>gi|27369724|ref|NP_766107.1| hypothetical protein 4932411M14 [Mus musculus]

gi|26325912|dbj|BAC26710.1| unnamed protein product [Mus musculus]
Length = 970

Score = 283 bits (724), Expect = 9e-75
Identities = 194/595 (32%), Positives = 300/595 (50%), Gaps = 50/595 (8%)

Query: 265 LFSPSDHRVPRIYVPLK--DCPQDFMTRPKDFANTLFICRIIIDWKEDCNFALGQLAKSLG 322
L +P D+R+P+I + + + QDF + RI W+ + G + LG
Sbjct: 283 LVTPWDYRIPKIRISTQQAEALQDFRV-----VVRIDSWEATSVYPNGHFVRVLG 332

Query: 323 QAGEIEPETEGILTEYGVDFSDFSSDEVLECLPQSL---PWTIPPDEVGKRRDLRKD-CIF 378
+ G++E E IL E + FS + +P + PW + P E +R+DLR +F
Sbjct: 333 RIGDLEGEIATILVENSISVVVFSEAQMCCEMPVNTPENPWKVSPKEEQRKDRLTTHLVF 392

Query: 379 TIDPSTARLDALACRRLTDGTFEVGVHIADVSYFPEGSSLKDVAERATSVYLVQKV 438
+IDP D+DD L+ R L +G E+GVHIADV++FV S +D A RAT+ YL +
Sbjct: 393 SIDPKGCEDVDDTLSVRTLNNGNLELGVHIADVTHFVAPNSYIDVEARTRATTYYLADRR 452

Query: 439 VPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPPEG-KILEEWFGRTIIRSCTKLSYDHAQS 497
MLP +L +LCNL D+ SV+W+L +I + W+GRTIIRS KL Y+ AQ
Sbjct: 453 YDMLPSILSADLCSSLGGVDRYAVSVMWELDKTSYEIKVWYGRTIIRSAYKLFYEAQE 512

Query: 498 MIENXXXXXXXXXXXXXXHS---VEEVHQAVLNLSIAKQLRRQRFVDGALRLDQLK 553
+++ S +EE+ A+ L IA+ +R +R GAL L+ ++
Sbjct: 513 LLDGNFSIVDDIPELKALDKQSQQAKLEELVWAIGKLTDIRHIRAKRDRCGALEGVE 572

Query: 554 LAFTLDHETGL----PQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRH 608
+ LD + + Q ++E V E M+LAN VA KI+ +FP QALLR+H
Sbjct: 573 VRVQLDDKKNIRDLPKQPLLEVHE----TVAECMILANHWAKKIWESFPHQALLRQH 626

Query: 609 PPPQTCKMLSDLVEFCDQMGLPMDVSSAGALNKS LT KTFGDDKYSLARKEVLTNMSRPMQ 668
PPP + S+L E G +D S L SL D K L K +L +M ++ M
Sbjct: 627 PPPHQEFFSELRECAKAKGFFIDTRSNKTLADSLDSA-NDPKDPLVNK-LLRSMATQAMS 684

Query: 669 MALYFCSGMLQDQEQRHYALNVPLYTHFTSPIRFADIVHRLAALGYSEQPDVEPD 728
ALYF +G +E+F HY L + YTHFTSPIRR++D++VHRL AA+ ++ +++ +
Sbjct: 685 NALYFSTGSCA-EEEFHHYGLALDKYTHFTSPIRYSDIVHRLMAAISKDKKMEIKEN 743

Query: 729 ----TLQKQADHCNDRRMASKRVQELSIGLFFAVLVKGPLESE----AMVMGVLNQ 778
L++ H N+R A++R Q+ S LF + K+ E ++ +
Sbjct: 744 LFSNKNLEELCRHINNRNRAAQRSQKQSTELFQCMYFKDRDAETEERCIADGVIYSIRTN 803

Query: 779 AFDVLVLRFGVQKRIYCNALALRSYSFQKVGKKPELTLWEPDDLEEEPTQQVIT 833
V + RFG++ Y L++ + PE + W+P L+ + + T
Sbjct: 804 GVLVFIPRGFIKGAAY----LKNKDSLVISCGPEGSSEWKGSLQRSQNKIIST 853

Score = 54.7 bits (130), Expect = 7e-06
Identities = 33/103 (32%), Positives = 54/103 (52%), Gaps = 8/103 (7%)

Query: 50 FETYMSKEDVSEGLKRGTLIQGVLRINPKKFH-EAFI----PSPDGD-RDIFIDGVVA 101
+ ++ E + G+K G IQG+L +N + EAF+ S D DI I G A
Sbjct: 142 YPEHLPLEVLEAGIKSGRYIQGILNVNKHRAQIEAFVRLHGASSKDSGLVSDILIHGSKA 201

Query: 102 RNRALNGDLVVVKLLPEDQWKAVKPESNDKEIEATYEADIPEE 144
RNR+++GD+VVV++LP+ +WK + + + + P E
Sbjct: 202 RNRSIHGDVVVEMLPKSEWKGRTAALGENSDDKASGESPSE 244

>gi|14250916|emb|CAC39263.1| putative ribonuclease II-like protein
[Trypanosoma brucei]
Length = 895

Score = 278 bits (710), Expect = 4e-73
Identities = 236/763 (30%), Positives = 352/763 (46%), Gaps = 109/763 (14%)

Query: 52 TYMSKEDVSEGLKRGTЛИQGVLRİ-NPKKFHEAFİPSPDGDRDIFIDGVVARNRALNGDL 110
T S ++ + +K G ++ G LR+ + AF+ S D+ + G + NR L+ D+
Sbjct: 18 TIGSNPEMEKQVKHGVVIGRLRVYSSYNSGLAFVRSGAFPADVVVKGYGSINRFLHNDV 77

Query: 111 VVVKLLPEDQWKAV----KPESNDKEIEATYEADİPEEGCGHHPLQQSRKGWSGPDVII 165
V V+LLP +QW+ V +P+ +DK+ T D L R+ I
Sbjct: 78 VAVQLLPMEQWEDVVSGELEPDGDDKDEFRTMRPD-----SERLPDGRR-----I 122

Query: 166 EAQFDDSDSEDRHGNNTSGLVGVKKLSISTPDRGKEDSSTPVMDENTPIPQDTRGLSEK 225
D+ +R L + +S P P
Sbjct: 123 TRWIRDTTMNNRKNREMWLAE-----MMSAPTEHNWHGKKP----- 158

Query: 226 SLQSAKVYYILEKKHSRAATGILKLLADKNSDLF--KKYALFSPSDHRVPRIYVPLKDC 283
S V+ +LE+KH L A + ++ +++ F D +P I V +D
Sbjct: 159 ----SGSVIAVLERKHPLLVARLADDALSSQEVIQDRRFYRFKVFQFDQLLPHIAVFGDI 214

Query: 284 PQDFMTRPKDFANTLFICRI-----IDWKEDCNFALGQLAKSLGQAGEIEPETEGILT 336
P F R + ++ R+ I W E F ++ + G + T I +
Sbjct: 215 P--FSLR-ESIRERFYLLRLETTGGDIVWAES-RFPTARIISTFGSVHSLRANTFAICS 270

Query: 337 EYGVDFSDFSSEVLECLPQSLPWTIPPDEVGK---RRDLRK-DCIFTIDPSTARLDLDDAL 392
+ + DFS E C+P L IP E K RRDLR+ + + +IDP+TARLDLDDAL
Sbjct: 271 AHHIVTDDFSEEACNCIPDRL--IIPNSEEMKRTGRRDLRREFVCSIDPATARLDLDDAL 328

Query: 393 ACRLTDGTFEVGVHIADVSYFVPEGSSLKVAERATSVYLVQKVVPMPLPRLLCEELCS 452
+ L G + VGVHIADVS+FV GS+LD+ RATSVYLV +V MLPR L EE CS
Sbjct: 329 SI-TLLPGGYRVGVHIADVSHFVSPGSALDEEGRARATSVYLDRVYHMLPRKLSEEVCS 387

Query: 453 LNPMTDKLTFSVIWKLTPEGKILEEWFGRTIIRSCTKLSYDHQSMIENXXXXXXXXX 512
L+P +DKL FS I++L GK+ EWFG+++IR+ +LSYD AQ +I+
Sbjct: 388 LHPGSDKLAFSAIFQLDLNGKLGEWFGKSVIRNRCRLSYDDAQRIIDGNLTLDALDYG 447

Query: 513 XXXXXHSVE---VHQAVLNLSIAKQLRRQRFVDGALRLDQLKLAFTLDHETG--LPQ 566
+ + V +V +L +A +LR F G L ++ F + + P
Sbjct: 448 GVTDRRELSQLKARVATSVKHLFDLASKLRAASFERGRLAFSTPEIGFHFEDISNPTHPI 507

Query: 567 GCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPQTKMLSDLVEFCDQM 626
G + + + +N LVEEFMLLAN+ VA KI + P+QA+LR HPPP+ L ++
Sbjct: 508 GFNVHRQIEANWLVEEFMLLANLRVAQKIVQYLPDQAILRVHPPPKRVPFEQL----KV 562

Query: 627 GLP-MDVSSAGALNKS LT KTFGDDKYSLARKEVLTNMYSRPMQM ALYFC SGM-LQDQE QF 684
L + + G N KSL + + R E + M + + A Y +G ++
Sbjct: 563 SLARVNIELKGRSNKSLEQLLNSVRDHPLRDEI-SIMVKNTLSLAKYCTNGENFTNKVPL 621

Query: 685 RHYALNVPLYTHFTSPIRFADIVHRLAAALGYSE-----QPDVEPDTL 730
HYAL + YTHFTSPIRR+AD+IVHR L AL +E + L
Sbjct: 622 GHYALGLEWYTHFTSPIRYADIIVHRQLLCALEIESIVKGKHRTGKTCA GAVGMEVECL 681

Query: 731 QKQ-----ADHCNDRRMASKRVQELSIGLFFAVLVK 761
AD CN+ + A+ V E S+ LFF +K
Sbjct: 682 DSAEFFTSTYEVNIADECNENKRAADSVSEASLKLFFCHYLK 724

>gi|15559519|gb|AAH14124.1|AAH14124 Unknown (protein for IMAGE:4561365)
[Homo sapiens]
Length = 647

Score = 270 bits (689), Expect = 1e-70
Identities = 178/534 (33%), Positives = 276/534 (51%), Gaps = 38/534 (7%)

Query: 315 GQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSL---PWTIPPDEVGKRRD 371
G + LG+ G++E E IL E + FS + +P + PW + P+E KR+D
Sbjct: 1 GTRVRVLGRIGDLEGIA TILVENSISVIPFSEAQMCEMPVNTPESPWKVSPEEQKRKD 60

Query: 372 LRKD-CIFTIDPSTARLDLDDALACRRLTDGTFEVGVHIADVSYFVPEGSSLKVAERAT 430
LRK +F+IDP D+DD L+ R L +G E+GVHIADV++FV S +D A RAT

Sbjct: 61 LRKSHLVFSIDPKGCEDVDDTLSVRTLNNGNLELGVIADVTHFVAPNSYIDIEARTRAT 120

 Query: 431 SVYLVQKVVPMPLPRLLCEELCSLNPMTDKLTFSVIWKLTPEG-KILEEWFGRTIIRSCTK 489
 + YL + MLP +L +LCSL D+ S++W+L +I + W+GRTIIRS K
 Sbjct: 121 TYYLADRRYDMLPSVLSADLCSSLGGVDRYAVSIMWELDKASYEIKKVWYGRTIIRSAYK 180

 Query: 490 LSYDHAQSMIENXXXXXXXXXXXXXXHS---VEEVHQAVLNLSIAKQLRRQRFVDG 545
 L Y+ AQ +++ S +EE+ A+ L IA+ +R +R G
 Sbjct: 181 LFYEAAQELLDGNLSVVDDIPEFKDLGEKSROAKLEELVWAIGKLTDIARHVRAKRDGCG 240

 Query: 546 ALRLDQLKLAFTLD----HETGLPQGCHIYEYRDSNKLVEEFMILLANMAVAHKIFRTFP 600
 AL L+ +++ LD H+ Q ++E V E M+LAN VA KI+ +FP
 Sbjct: 241 ALELEGVEVCVQLDDKKNIHDLIPKQPLEVHE----TVAECMILANHWVAKKIWESFP 294

 Query: 601 EQALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKS LT KTFGDDKYSLARKEVLT 660
 QALLR+HPPP + S+L E G +D S L SL +D + +L
 Sbjct: 295 HQALLRQHPPPQEFFFSELRECAKAKGFFIDTRSNKTLADSLDN--ANDPHDPIVNRLLR 352

 Query: 661 NMYSRPMQMAMYFCGMLQDQEQRHYALNVPLYTHFTSPIRFADIVHRLLLAAALGYS 720
 +M ++ M ALYF +G +E+F HY L + YTHFTSPIR++D++VHRLL AA+
 Sbjct: 353 SMATQAMSNALYFSTGSCA-EEEFHGYGLALDKYTHFTSPIRYS DIVVHRLLMAAISKD 411

 Query: 721 EQPDVEPD----TLQKQADHCNDRRMASKRVQELSIGLFFAVLVKESGPLE----SEA 770
 ++ +++ + L++ H N+R A++ Q+ S LF + K+ P S+
 Sbjct: 412 KKMEIKGNLFSNKDLEELCRHINNRNQAAQHSQKQSTELFQCMYFKDKDPATEERCISDG 471

 Query: 771 MVMGVLNQAFDVVLVRFGVQKRIYCNALALRSYSFQKVGGKPELTLVWEPPDLE 824
 ++ + + RFG++ Y L++ + P+ W+P L+
 Sbjct: 472 VIYSIRTNGVLLFIPRGFIKGAAY----LKNKDGLVISCGPDSCSEWKPGSLQ 520

>gi|23136616|gb|ZP_00118334.1| hypothetical protein [Cytophaga hutchinsonii]

Length = 750

Score = 265 bits (676), Expect = 3e-69

Identities = 168/466 (36%), Positives = 252/466 (54%), Gaps = 35/466 (7%)

Query: 315 GQLAKSLGQAGEIEPETEGILTEYGVDFSDSSEVLECLPQSLPWTIPPDEVGKRRDLRK 374
 G++ + LG AGE E E IL E+G+ + +F ++V++ Q + E+ KRRD+R
 Sbjct: 219 GKVTEVLGMAGENETEMHAILAEFGLPY-EFPNQVIKA-AQDITAETSEAEIKKRRDMRG 276

Query: 375 DCIFTIDPSTARLDALACRRLTDGTFEVGVIADVSYFVPEGSSLKVAERATSVYL 434
 FTIDP A+D DDA++ + L +G +E+GVHIADVS++V G +LDK A RATSVYL
 Sbjct: 277 TTTFTIDPEDAKDFDAISFKYLDNGNWEIGVHIADVSHYVQPGDTLDKEAYRRATSVYL 336

Query: 435 VQKVVPMPLPRLLCEELCSLNPMTDKLTFSVIWKLTPEGKILEEWFGRTIIRSCTKLSYDH 494
 V + VPMLP L ELCSL P DKLTF S I++ + K+L+EWFGRTII S + SY+
 Sbjct: 337 VDRCVPMLPERLSNELCSLRPNEDKLTFSAIFEIDADAKVLDEWFGRTHIHSSTRFSYEQ 396

Query: 495 AQSMIENXXXXXXXXXXXXHSVEEVHQAVLNLSIAKQLRRQRFVDGALRLDQLKL 554
 AQ +IE + + + L+++AK++R QRF +GA+ + +++
 Sbjct: 397 AQEVVIETQQG-----DLVKELTILNTLAKKMRAQRFKEGAISFETVEV 439

Query: 555 AFTLDHETGLPQGCHIYEYRDSNKLVEEFMILLANMAVAHKIF----RTFPEQALLRRHP 609
 F LD + G P +D++KL+EEFMLAN VA +F + + R H
 Sbjct: 440 KFQLDAK-GKPLAVVVKVRDAHKLIEEFMLLANKRVAEFVFNLRLKGKGTTSNTMVYRTHD 498

Query: 610 PPQTKMLSDLVEFCDQMGLPMDVSSAGALNKS LT KTFGDDKYSLARKEVLTNMSRPMQM 669
 P + L+ L F + G +++ A+ K+L K D+ + VL ++ R M
 Sbjct: 499 APNPEKLASLATFAKRGFGKVELDDENAIAKNLNK-LSDEVEGKPEQNVLQSLAIRTMSK 557

Query: 670 ALYFCGMLQDQEQRHYALNVPLYTHFTSPIRFADIVHRLLLAAALGYS EQPDVEPDT 729
 A+Y E H+ L Y+HFTSPIR+ DV+ HRLL L + D E
 Sbjct: 558 AIY-----SIEPDMHGLAFKHYSHTSPIRYPDVMARLLQHYLDGGKSADKE--Y 608

Query: 730 LQKQADHCNDRRMASKRVQELSIGLFFAVLVKESGPLESEAMVMGV 775
+ +H + + + SI ++ S E E +V GV
Sbjct: 609 YIEACEHSSAQEKLAEEAERSSIKFKQVEFMQSSIGKEFEGIVSGV 654

>gi|19173030|ref|NP_597581.1| similarity to DIS3 PROTEIN (RNASE II FAMILY)
[Encephalitozoon cuniculi]
gi|19168697|emb|CAD26216.1| similarity to DIS3 PROTEIN (RNASE II FAMILY)
[Encephalitozoon cuniculi]
Length = 835

Score = 260 bits (665), Expect = 6e-68
Identities = 161/460 (35%), Positives = 240/460 (52%), Gaps = 64/460 (13%)

Query: 265 LFSPSDHRVPRIYVPLKDCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQA 324
L P D R+P I + ++ ++ N I W+ N+ G + LG
Sbjct: 288 LVIPIDRRIPAIRIR-----TSQAEELMNKRLCVEIDGWERTSNYPSGHYYRRLGTL 339

Query: 325 GEIEPETEGILTEYGVDFSDFS-SEVLECLPQSLPWTIPP-----DEV--GKRRDLR 373
G+ E E +L G+ + + +E+L +PW +EV G R D R
Sbjct: 340 GDRNAEMEAVLVANGITYYNKNWAEILR----VPWMNEDIFGMEMKAYNEVREGTREDFR 394

Query: 374 KDCIFTIDPSTARLDLACRRLTDGTFEVGHIADVSYFVPEGSSLKDVAERATSVY 433
+ I +IDP D+DDAL CR L +G +EVGHIADV+Y+V +GS +DK+AA+R T++Y
Sbjct: 395 ELSIVSIDPPDCEDIDDALHCRLLPNGNWEVGHIADVTYYVTKGSEIDKIAADRGTTIY 454

Query: 434 LVQKVVPMPLPRLLCIELCSLNPMTDKLTFSVIWKLTPEGKILEEWFGRTIIRSCTKLSYD 493
L + + MLP L +LCSL D+ FSV+W+++ + +++ F R++IRS SY+
Sbjct: 455 LPEWRIDMLPPALSTDLCISLVAGKDRAAFSVVWEMSSDVRVVRTHFCRSLIRSKRSFSYN 514

Query: 494 HAQSMIENXXXXXXXXXXXXXXHSVEEVHQAVLNLSIAKQLRRQRFVDGALRLDQLK 553
A ++ +EV +++ L I++ LR +RF G+L L +
Sbjct: 515 EAYDAVQGLVDAG-----DEVSRSRMLLEISRVLRSRRFAKGSDLSTRQ 560

Query: 554 LAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQT 613
L F G + EY +N LVEEFM+LAN++VA I+ P+ +LLR+HPPP
Sbjct: 561 LVFR-----EGGFEMKEYFPTNFLVEEFMLANISVASFIYHHHPDSSLRKHPPPSV 613

Query: 614 KMLSDLVEFCDQMGLPMDVSSAGALNKS LT KTFGDDKYSLARKEVLTNMYSRPMQMAYF 673
+GL +D SS AL++SL K G RK++ M R M A+Y
Sbjct: 614 L-----DIGLDIDTSSPRALSELEKMEG-----VRKDLAKRMLIIRSMNQAVYV 657

Query: 674 CSGMLQDQEQRHYALNVPLYTHFTSPIRFADIVHRL 713
SG + HY L P+YTHFTSPIRR+AD+IVHR+L
Sbjct: 658 VSG---ETPSLHHYGLATPIYTHFTSPIRRYADIIVHRL 694

>gi|7493807|pir||T30524 protein phosphatase Ssd1 homolog - yeast (Candida albicans)
gi|2459997|gb|AAC83386.1| protein phosphatase Ssd1 homolog [Candida albicans]
Length = 1262

Score = 246 bits (628), Expect = 1e-63
Identities = 230/859 (26%), Positives = 391/859 (45%), Gaps = 86/859 (10%)

Query: 49 IFETYMSKEDVSEGLKRGTLIQGVLRINPKKFHEAFIPSPDG--DRDIFIDGVVARNRAL 106
+F Y+ + + E + G L+ G LR+N K +A++ S DG D DIFI G RNRAL
Sbjct: 336 LFAPYLPQSSLPELINEGRLVGTLRVNKKNRSDAYV-STDGLLDADIFICGSKDRNRAL 394

Query: 107 NGDLVVVKLLPEDQ-WKAVKPESNDKEIEATYEADIPPEEGCGHHPLQQSRKGWSGPDVII 165
GDLV V+LL D+ W++ K + K + P H+ S P+
Sbjct: 395 EGDLVAVELLIVDEVWESKKEKEKKRRKDNTLHSRPLTDDIH-----DATSAPNT-A 447

Query: 166 EAQFDDSDSED RHGNTSGLVDGVKKLSISTPDRGKEDSSTPVMDENTPIP-QDTRGLSE 224

E + ED G+ G+ + RG + K+++ + Q + E
 Sbjct: 448 EGSVTGTSKEDGAGSNEEETGGLAR-----RGSLKQRPTMKKNDDVEVEGQSLLLVEE 500

Query: 225 KSLQKSAK-----VVIYLEKKHSRAATGILKLL-----ADK-----NSDLFK 261
 + + K VV +++++ + G L LL DK +

Sbjct: 501 EEINDEIKPLYAGHVAVVDRIPGQLFAGTLGLLRPAQAAQAARDKKNGKESTVQNPKAP 560

Query: 262 KYALFSPSDHRVPRIYVPLKDCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSL 321
 K F P+D +VP I +P + P+DF+ + +A+ LF+ I W GL +L

Sbjct: 561 KIVWFKPTDKVPLIAIPTEQAPKDFVENHEKYADRRLFVASIKRWPITSLHPFGTLVSNL 620

Query: 322 GQAGEIEPETEGILTEYGVDFSDFS---SEVLECLPQSLPWTIPPDEVGKRRDLRKDCI 377
 G E E + IL + ++ +++ LP P E +R + D I

Sbjct: 621 GPIDSPETEIDSILRDNNFLCDEYPDDDNDIVSVNAYDLPSIEPEFENTQREEYLNDYI 680

Query: 378 FTIDPSTARLDALACRRLTDGTFEVGVIADVSYFVPEGSSLKVAERATSVYLVQK 437
 +D AL +R+++ E+G H+AD++YF+ GSLLD+ + +R++SV+L QK

Sbjct: 681 IAFT-QNGEFVDHALHVKRISNTKIELGFHVADIAYFIKPGSSLDRKSKKRSSSVFLPQK 739

Query: 438 VVPMPLPRLLCEELCSLNPMTDKLTFSVIWKL-TPEGKILEEWFGRTIIRSCTKLSYDHAQ 496
 V + P+ + ++ S L SV++++ T ++ + + ++I ++YD

Sbjct: 740 TVNLFPKQV-NKIVSFKENEKNLAVSVFEDTSNFEVEDLYIHESVIIPKQLVTDYAFD 798

Query: 497 SMIENXXXXXXXXXXXXXXHSVEEVHQA---VLNLHSIAKQLRRQRFVDGALRLD-Q 551
 +++ SV+ + A V IAK+ RR R + +L +

Sbjct: 799 TILSG-----QSVDSISSATSDYVKTFSLIKEFRRHRLSNRSLGITPN 842

Query: 552 LKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPP 611
 L L LD E + +I++ + ++ E N A+A K+ +QA+LRRHP P

Sbjct: 843 LTLLDQLDDEK-VRLDLNIFKDSDLAFDVISEISHKVNSAIAAKVHAGLGDQAILRRHPLP 901

Query: 612 QTKMLSDLVEFCQMDLPMDVSSAGALNKS LT KTFGDDKYSLARKEVLTNMYSRPMQMAL 671
 + + V +G +D +++ L S+ K DD + RK V T +Y + M

Sbjct: 902 TLQKMETFVRKATSLGFKIDTTSSLQNSILKI--DD--PVKRKCETLLY-KCMSRGR 956

Query: 672 YFCSGMLQDQEQRHYALNVPLYTHFTSPIRFADIVHRLLAAALGYSEQPDVEPDTLQ 731
 Y+ +G QD + + HY N+PLYTHFT+P+RR+AD+IVHR L A L + D + D+L+

Sbjct: 957 YYVAGK-QDTDSYAHYYFNLPYTHFTAPLRRYADLIVHRQLKAVLN-KQVEDKDLSLK 1014

Query: 732 KQADHCNDRRMASKRVQELSIGLFFAVLVKESGPLESEAMVMGVLNQ---AFDVLVLRF 787
 D+CN ++ + QE +I L + + E + + MG + Q +FDV + F

Sbjct: 1015 AITDYCNFKKDCAANAQEQAIIHLLSQTINEMSETAGQLLCMGTVVQVYESSFDVFIPEF 1074

Query: 788 GVQKRIYCNALALRSYSFQKVGKKPELTLWEP--DDLEEEPTQQVITIFSLVDVVLQAE 845
 GV+KR++ + L L F K + L L WE D P + ++ + +

Sbjct: 1075 GVEKRVHGDQLPLVKAEDK--NERILELWWEKGVDSATYIPPDEKSSLSYRNSIKNKYR 1132

Query: 846 ATALKYSAILKRPGLEKAS 864
 +AL+ + I + LEK++

Sbjct: 1133 TSALQAAKIQSKTALEKST 1151

>gi|22748821|ref|NP_689596.1| hypothetical protein MGC42174 [Homo sapiens]
 gi|20988352|gb|AAH30113.1| similar to Hypothetical 93.7 kDa protein
 F48E8.6 in chromosome III
 [Homo sapiens]
 Length = 159

Score = 242 bits (617), Expect = 2e-62
 Identities = 119/135 (88%), Positives = 127/135 (94%)

Query: 727 PDTLQKQADHCNDRRMASKRVQELSIGLFFAVLVKESGPLESEAMVMGVLNQAFDVLVLR 786
 PDTLQKQADHCND RMASKRVQELS LFFAVLVKESGPLESEAMVMG+L QAFDVLVLR

Sbjct: 3 PDTLQKQADHCND SRMASKRVQELSTS LFFAVLVKESGPLESEAMVMGILKQAFDVLVLR 62

Query: 787 FGVKRIYCNALALRSYSFQKVGKKPELTLWEPDDLEEEPTQQVITIFSLVDVVLQAEA 846

+GVQKRIYCNALALRS+ FQKVGKKPELTLVWEP+D+E+EP QQVITIFSLV+VVLQAE
Sbjct: 63 YGVQKRIYCNALALRSHFQKVGGKPELTLVWEPEDEMEQEPAQQVITIFSLVEVVLQAEY 122

Query: 847 TALKYSAILKRPGL 861
TALKYSAILKRPGL +
Sbjct: 123 TALKYSAILKRPGTQ 137

>gi|27685983|ref|XP_237349.1| similar to hypothetical protein MGC37640 [Mus
musculus] [Rattus
norvegicus]
Length = 1034

Score = 241 bits (614), Expect = 5e-62
Identities = 117/128 (91%), Positives = 121/128 (94%), Gaps = 2/128 (1%)

Query: 188 VKKLSISTPDRGKEDSSTPVMKDENTPI PQDTRGLSEKSLQSAKVVYILEKKHSRAATG 247
+KK+S S+ DR KEDSS PVMKDENTP QDTR LSEKSLQSAKVVYILEKKHSRAATG
Sbjct: 509 LKKIS-SSNDR-KEDSSAPVMKDENTPKSQDTRALSEKSLQSAKVVYILEKKHSRAATG 566

Query: 248 ILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFMTRPKDFANTLFICRIIDWK 307
ILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFMTRPKD+ANTLFICRIIDWK
Sbjct: 567 ILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFMTRPKDYANTLFICRIIDWK 626

Query: 308 EDCNFALG 315
EDCNFALG
Sbjct: 627 EDCNFALG 634

Score = 142 bits (357), Expect = 3e-32
Identities = 64/80 (80%), Positives = 70/80 (87%)

Query: 122 KAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSPDVIIEAQFDDSDSEDRHGNT 181
+ VKPESNDKE EAT E DI EE CGHH LQ+S KGW+GPDVIIEAQFDDSDSEDRHGNT
Sbjct: 328 RGVKPESNDKETEATNETDISEESCGHLLLQKSPKGWNGPDVIIEAQFDDSDSEDRHGNT 387

Query: 182 SGLVDGVKKLSISTPDRGKE 201
SGLVDG+KKLS+ TPD+G E
Sbjct: 388 SGLVDGMKKLSVCTPDKGSE 407

Score = 127 bits (320), Expect = 6e-28
Identities = 58/62 (93%), Positives = 60/62 (96%)

Query: 316 QLAKSLGQAGEIEPETEGILTEYGVDFSDSSEVLECLPQSLPWTIPPDEVGKRRDLRKD 375
QLAKSLGQAGEIEPETEGILTEYGVDFSDSSEVLECLPQSLPWTIPP+EVGKRRDLR
Sbjct: 724 QLAKSLGQAGEIEPETEGILTEYGVDFSDSSEVLECLPQSLPWTIPPEEVGKRRDLRSL 783

Query: 376 CI 377
C+
Sbjct: 784 CL 785

Score = 117 bits (292), Expect = 9e-25
Identities = 52/57 (91%), Positives = 57/57 (100%)

Query: 68 LIQGVLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNGDLVVVKLLPEDQWKAV 124
+++GVLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNGDLVVVKLLPEDQWK++
Sbjct: 205 VLKGVLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNGDLVVVKLLPEDQWKSL 261

Score = 60.1 bits (144), Expect = 2e-07
Identities = 25/28 (89%), Positives = 28/28 (100%)

Query: 373 RKDCIFTIDPSTARLDLACRRLTDG 400
+KDCIFTIDPSTARLDLACRRLTDG

Sbjct: 867 QKDCIFTIDPSTARLDALSCRQLTDG 894

>gi|6320499|ref|NP_010579.1| Product of gene unknown; Ssd1p [Saccharomyces cerevisiae]
gi|134917|sp|P24276|SSD1_YEAST SSD1 PROTEIN (SRK1 PROTEIN)
gi|101639|pir||A39578 SSD1 protein - yeast (Saccharomyces cerevisiae)
gi|172612|gb|AAA35047.1| SSD1 protein
gi|172697|gb|AAA35089.1| SRK1
gi|1230657|gb|AAB64469.1| Ssd1p [Saccharomyces cerevisiae]
Length = 1250

Score = 221 bits (564), Expect = 3e-56
Identities = 227/823 (27%), Positives = 369/823 (44%), Gaps = 95/823 (11%)

Query: 49 IFETYMSKEDVSEGLKRGTLIQQVLRINPKKFHEAFIPSPDG--DRDIFIDGVVARNRAL 106
+F Y+ + ++ E ++ G L+ G+LR+N K +A++ S DG D DI+I G RNRAL

Sbjct: 340 LFAPYLPQANIPELIQEGRLVAGILRVNKKNRSDAWV-STDGALDADIYICGSKDRNRAL 398

Query: 107 NGDLVVVKLL-PEDQWKA-VKPESNDKEIEATYEADIPPEEGCGHPLQQSRKGWSGPDVI 164
GDLV V+LL +D W++ + E + +A+ + D+ PL S + V

Sbjct: 399 EGDLVAVELLVVDDWESKKEKEEKRRKDASMHQHDLI-----PLNSSDDYHNDASVT 451

Query: 165 IEAQFDDSDSEDRHGNTSGLVDGVKKLSISTPDRGKEDSSTPV-----MKDENTPI 215
+ S + S V++ ST + + S+P +K T

Sbjct: 452 AATSNNFLSSPSSSDSLSKDDLSVRRKRSSTINNDSDSLSSPTKSGVRRRSSLKQRPTQK 511

Query: 216 PQDTRGLSEKSL-----QKSAKVVYILEKKHSRAATGILKLL---ADKN SD 258
D + +SL + VV +L++ + +G L LL NSD

Sbjct: 512 KNDDVEVEGQSLLLVEEEEINDKYKPLYAGHVVAVLDRIPGQLFSGTLGLLRPSQQANS 571

Query: 259 LFK----KYALFSPSDHRVPRIYVPLKDCPQDFMTRPKDFANTLFICRIIDWKEDCNFA 313
K K A F P+D +VP I +P + P+DF+ ++ LF+ I W

Sbjct: 572 NNKPPQSPKIAWFKPTDKKVPLIAIPTELAKDFVENADKYSEKLFVASIKRWPITS 631

Query: 314 LGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLEC-----LPQLPWTIPPDEVG 367
G L LG + + E + IL D + S+E L+ P P + + +

Sbjct: 632 FGILVSELGDIHDPTDEIDSILR---DNNFLSNEYLDQKNPKEKPSFQPLPLTAESLE 687

Query: 368 KRR---DLRKDCIFTIDPSTARLDALACRRLTDGTFEVGVHIADVSYFVPEGSSLKV 424
RR D + IF I + AL R +GT E+G H+ DV+ + EGSS+D+

Sbjct: 688 YRRNFTDTNEYNIFAIS-ELGWVSEFALHVRNNNGNTLELGCHVVDVTSHIEEGSSVDR 746

Query: 425 AAERATSVLVQKVVPMPLPRLLCEELCSLNPMTDKLTFSVIWKLTPEG-KILEEWFGRTI 483
A +R+++V++ QK+V +LP+ +EL SL P + T SV++ L +I W G +

Sbjct: 747 ARKRSSAVFMPQKLVNLLPQSFNDEL-SLAPGKESATLSVVTLDSSLRIKSTWVGEST 805

Query: 484 IRSCTKLSYDHQAQSMIENXXXXXXXXXXXXHSVEEVHQAVLNLSIAKQLRRQRFV 543
I LS + + S + + IA+ +R

Sbjct: 806 ISPSNILSLEQLDEKL-----STGSPTSYLSTVQEIARSFYARRIN 846

Query: 544 D-GALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQ 602
D A L L'L +LD E + +I + ++ E N VA KI+ +

Sbjct: 847 DPEATLLPTLSLLESLDDEK-VKVDLNILDRTLGFVVINEIKRKNSTVAEKIYT KLGDL 905

Query: 603 ALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKS LT KTFGDDKYSLARKEVLTNM 662
ALLRR P ++ + G D ++A L K + K DD R + +

Sbjct: 906 ALLRRQMQPIATKMASFRKKIQNFGYNFDTNTADELIKGVLKIKDDD---VRVGIEILL 961

Query: 663 YSRPMQMALYFCGMLQDQEQRHYALNVPLYTHFTSPIRFAADVIVHRLLAALGYSEQ 722
+ + M A YF +G + D +Q+ HYALN+P+YTHFT+P+RR+AD +VHR L A + +

Sbjct: 962 F-KTMRARYFIAGKV-DPDQYGHYALNLPIYTHFTAPMRRYADHVVHRQLKAVI--HDT 1017

Query: 723 PDVEP-DTLQKQADHCNDRRMASKRVQELSIGLFFAVLVKE---SGPLESEAMVMGVLN 777
P E + L+ +++CN ++ + + QE + I L + + +G L + A V+ V

Sbjct: 1018 PYTEDMEALKITSEYCNFKDCAYQAQEQAIIHLLCCTINDMGNTTGQLLTMATV LQVYE 1077

Query: 778 QAFDVLVLRGVQKRIYCNALALRSYSFQKVGGKPELTWEP 820
+FDV + FG++KR++ + L L F G L L W+P

Sbjct: 1078 SSFDVFIPEFGIEKRVHGDQLPLIKAED--GTNRVLELHWQP 1118

>gi|15616115|ref|NP_244420.1| ribonuclease R; virulence-associated protein [Bacillus halodurans]

gi|25298858|pir||A84094 virulence-associated protein BH3553 [imported] - Bacillus

halodurans (strain C-125)

gi|10176177|dbj|BAB07272.1| ribonuclease R [Bacillus halodurans]
Length = 771

Score = 214 bits (545), Expect = 5e-54

Identities = 163/515 (31%), Positives = 250/515 (48%), Gaps = 47/515 (9%)

Query: 232 KVYYILEKKHSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFMTRP 291

KV+ ILE R + ++ D + Y L D R+P + + Q +

Sbjct: 127 KVIKILE---RGVSEVIGTYVDHQT----YGLVVADDKRIPNDILIVNPEAQGLVDGH 177

Query: 292 KDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDSSEVLE 351

K I +I + E A G++ LG + + I+ +YG+ F EVL+

Sbjct: 178 K-----VIVKITKYPEGRMSAEGEVISILGHKNDPGMDILSIIYKYGIP-QAFPEEVLQ 230

Query: 352 CLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARLDALACRRLTDGTFEVGVHIADV 411

Q++P I E+ RRDLR + + TID + A+DLDDA+ RL +G F++GVHIADV

Sbjct: 231 -QAQNIPDEIDAGEIKNRRDLRDEPLVTIDGADAKDLDDAVHVSRLPNGNFKLGVHIADV 289

Query: 412 SYFPPEGSSLDKVAERATS VYLVQKVVPMPLRLLCEELCSLNPM TDKLTF SVIWKLTPE 471

SY+V E S +D AAER TSVYLV +V+PM+P L +CSLNP D+LT S ++T +

Sbjct: 290 SYYVKEKSPIDLEAAERGTS VYLVDRVIPMI PHRLSNGICSLNPQVDRTLSCEMEITRD 349

Query: 472 GKILEEWFGR TIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXHSVEEVHQAVLNH 531

G+++ +++IR+ +++Y ++ +EE

Sbjct: 350 GQVNHEIFQS VIRTNERMTYHDVN KILVEKEEE LRNRYELLVPMFEDMEE----- 400

Query: 532 SIAKQLRRQR FVDGALR LDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFML LANMAV 591

+A LR++RF GA+ D K A L E G P I E + KL+EE FML AN V

Sbjct: 401 -LAA ILRK KRG RAIDFD-FKEAKVLVDEEGKP SDVVIR ERGVAEKLIEE FMLAANETV 458

Query: 592 AHKIFRTFPEQ ALLRRH PPPQT KMLSDLVEFC DQM GLPMDVSSAG ALNKS LT KTFGDD KY 651

A F + R H P ++ L +EF G + ++ ++L K ++

Sbjct: 459 AEH-FH WLKL PFM YRIH EDPD SEK LGR FLE FITNFGY VVR GTANTV HPR ALQ KLL-EE VR 516

Query: 652 SLARKEVLT NMYSRPMQ M ALYFC SGML QDQE QFRHY ALNV PLYTHFT SPI RFA DVIV HR 711

++V++ + R MQ A Y D H+ L+ YTHFTSPI R+ D+IV HR

Sbjct: 517 GEPEEQVISTVMLRSMQQAKY-----DPTSLGHFGLSTEFYTHFTSPI RRY PDLIV HR 569

Query: 712 LLAA ALGYSEQPD VEPDTLQKQ-----ADHC ND 739

L+ Y + +V+ +T +K A HC++

Sbjct: 570 LIRE---Y LIKGNV DEETQ EKWRERLPEI ARHC SE 601

>gi|23099883|ref|NP_693349.1| ribonuclease R [Oceanobacillus iheyensis]

gi|22778114|dbj|BAC14384.1| ribonuclease R [Oceanobacillus iheyensis]

Length = 744

Score = 209 bits (533), Expect = 1e-52

Identities = 140/418 (33%), Positives = 214/418 (51%), Gaps = 22/418 (5%)

Query: 300 ICRI IDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDSSEVLECLPQSLPW 359

I RI + E N A G++ LG + + I+ ++G+ DF +VLE Q P

Sbjct: 183 IARISKYPEGRNSAEGEIIHILGHKNDPGIDILSIIHKHGIQV-DFPEDVLE-QAQQTPE 240

Query: 360 TIPPDEVGKRRDLRKDCIFTIDPSTARLDALACRRLTDGTFEVGVHIADV SYFVPEGS 419

I PDE+ RRDLR + I TID + A+DLDDA+ ++L++G +++GV+IADVS++V E S

Sbjct: 241 EIHPEINGRRDLRNETIVTIDGADAKDLDDAVTVKKLSNGNYKLGVYIADVSHYVKEES 300

 Query: 420 SLDKVAEARATSVYLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPLEGKILEEWF 479
 +D+ A ER TSVYLV +V+PM+P L +CSLNP D+LT ++ +G+++E

 Sbjct: 301 PIDREALERGTSVYLVDRVIPMIPHRLSNGICSLNPKVDRRTLGC EMEINHQGQVVEHEI 360

 Query: 480 GRTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXHSVEEVHQAVNLHSIAKQLRR 539
 +++I S +++Y ++ + +E NL SI LR

 Sbjct: 361 FQSVIHSTERMTYSDVNKILVDQDEELRDKYEPLVPMFEEME-----NLASI--LRE 410

 Query: 540 QRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTF 599
 +RF GA+ D K A L + G P I E + +L+EEFML AN +A F

 Sbjct: 411 KRGFRGAIDFD-FKEAQVLVDDMGRPTDVAIRERSVAERLIEEFMLAANETIAEH-FHWM 468

 Query: 600 PEQALLRRHPPPQTKMLSDLVEFCDFQMGLPMDVSSAGALNKS LT KTFGDDKYSLARKEVL 659
 + R H P L +F +G+ + +AG ++ + D + ++

 Sbjct: 469 DVPFIHRIHEEPDEGKLEKFFDFLAGLGISVK-GTAGDIHPQELQKVIDSIRGEPEEMIV 527

 Query: 660 TNMYSRPMQM ALYFCSGMLQDQEQRHYALNVPLYTHFTSPIRRFADVIVHRLAAL 717
 + + R MQ A Y D + H+ L YTHFTSPIRR+ D+IVHRL+ L

 Sbjct: 528 SKLMLRSMQQAKY-----DPQSIGHFGLATDFYTHFTSPIRRYPDLIVHRLIRTYL 578

>gi|21673344|ref|NP_661409.1| ribonuclease II family protein [Chlorobium tepidum TLS]
gi|21646438|gb|AAM71751.1| ribonuclease II family protein [Chlorobium tepidum TLS]
Length = 720

Score = 208 bits (529), Expect = 4e-52
Identities = 155/466 (33%), Positives = 233/466 (50%), Gaps = 57/466 (12%)

Query: 265 LFSPSDHRV-PRIYVPLKDCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQ 323
 L P ++ P I++PLK + K A L + ++ + LG
Sbjct: 154 LLKPDQRKILPEIHIPLKAKKAKAG-DKVLAGELEFLK-----SGTIQARVIEILGT 205

Query: 324 AGEIEPETEGILTEYGVDFSDSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPS 383
 AGE + E I G+D F E+L + + I +++ +R D+R +FTIDP
Sbjct: 206 AGESQVEVSAIARGLGID-ETFEPELL-TFAEKVREAITDEDLKERLDIRDKDVF TIDPV 263

Query: 384 TARLDL DALACRRLTD-GT FEVGVHIA DVSYFVPEGSSL DKVAAERAT SVYLVQKV VPML 442
 A+D DDAL+ L + G ++ VGVHIA DV+S+VPE S+LDK A +RAT SVYLV +V+PML
Sbjct: 264 DAKDFDDALSIE TLNGGGYKVGVHIA DVSHYVPENSALDKEARKRAT SVYLVDRV I PML 323

Query: 443 PRLLCEELCSLNPMTDKLTFSVIWKLTPLEGKILEEWF GRTIIRSCTKLSYDHAQSMIENX 502
 P L E++CSLNP D+L FSV + +T +G++ + F +T+I S + +Y+ Q +++
Sbjct: 324 PSRLSEKVC SLNPGVDR LAFSVFFNITKKGEVT KFEFHKT VIHSKRRFTYEDVQQILDAG 383

Query: 503 XXXXXXXXXXXXXXXHSVEEVHQAVNLHSIAKQLRRQRFVDGALRLDQLKLAFTLDHET 562
 + + + L ++K++R QR G L + ++ F L
Sbjct: 384 KG-----DYFRELQALDQLSKKIRAQRMESGGLEFETEEVRFKLG-SN 425

Query: 563 GLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTF-----PEQALLRRHPPPQTKML 616
 G P E DS++L+EEFMLAN VA + + P + R H PQ + +
Sbjct: 426 GEPVEVIKKERLD SHRLIEEFML LANRTVAAYLTARYAENEKN PHPVIYRVHGAPQMEKV 485

Query: 617 SDLVEFCDQMGLPMDVSSAG-----ALNKS LT KTFGDDKYSLARKEVLT NMYSRPM 667
 L F ++G + + G AL + L K G + L + VL R M
Sbjct: 486 QVLASFVRKIGFDLK LDRKGKDSATVSSKALRELLQKVR GTNVEFLV NELVL----RSM 540

Query: 668 QM ALYFCSGMLQDQEQRHYALNVPLYTHFTSPIRRFADVIVHRL 713
 A+Y L D H+ L YTHFTSPIRR+ D+IVHRL+
Sbjct: 541 SKAVY---SPLNDG---HFGLGF EH YTHFTSPIRRYPDLIVHRL 579

>gi|15672924|ref|NP_267098.1| ribonuclease [Lactococcus lactis subsp. lactis]

gi|18202798|sp|Q9CH00|RNR1_LACLA Ribonuclease R 1 (RNase R 1) (VacB protein homolog 1)
gi|25298855|pir||F86742 ribonuclease [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
gi|12723878|gb|AAK05040.1|AE006328_8 ribonuclease [Lactococcus lactis subsp. lactis]
Length = 817

Score = 206 bits (525), Expect = 9e-52
Identities = 137/421 (32%), Positives = 223/421 (52%), Gaps = 27/421 (6%)

Query: 315 GQLAKSLGQAGEIEPETEGILTEYGVDFSDSSEVLECLPQSLPWTIIPPDEVGKRRDLRK 374
G + + +GQA + + +L + S+F EVL+ +++P +P +E+ R D R
Sbjct: 207 GLVTEIIIGQADDQGIDVLEVLASMDI-VSEFPKEVLD-QAEAVPEEVPENEIVGRVDYRN 264

Query: 375 DCIFTIDPSTARLDLDDALACRRLTDGTFEVGVIADVSYFVPEGSSLKDVAERATSVYL 434
+ FTID + A+DLDDA+ +RL +G +E+GVHIADVS++V E S LDK A ER TSVY+
Sbjct: 265 EITFTIDGADAKDLDDAVHAKRENGNYELGVHIADVSHYVTENSPLDKEAYERGTSVYV 324

Query: 435 VQKVVPMPLRLLCEELCSLNPMTDKLTFSVIWKLTPEGKILEEWFGRTIIRSCTKLSYDH 494
+VVPMLP L +CSLNP ++LT S + +++PEG+++ ++II++ +++YD
Sbjct: 325 TDRVVPMLPERLSNGICSLNPRINRLTQSCVMEISPEGRVINYQISQSIIKTTERMYDA 384

Query: 495 AQSMIENXXXXXXXXXXXXXXHSVEEVHQAVNLHSIAKQLRRQRFVDGALRLDQLKL 554
MI + + + ++ LH I + +R++R GA+ D ++
Sbjct: 385 VNQMIAGDEAALENYA-----KIADSVKIMVELHHILEAMRKRR---GAIDFDTVE- 432

Query: 555 AFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQTK 614
A + +E GLP + +++E FML AN VA F + R H P+
Sbjct: 433 AKIIVNEKGLPIEIRKRTRGIAERMIESFMLEANETVATH-FEAHGLPFIYRIHEQPKAD 491

Query: 615 MLSDLVEFCDQMGLPMDVSSAGALNKS LT KTFGDDKYSLARKEVL TNMYSRPMQM ALYFC 674
L ++F G+ ++ +S G +++ + + F + VL+ M R MQ A Y
Sbjct: 492 RLQRFDFAATFGMQIEGT SNG-IDQKVLQAFM KKIKGQP GEMVLSTM LLRSM QQARY-- 548

Query: 675 SGMLQDQE QFRHYALNVPLYTHFTSPIRFADIVVH RLLAA ALGYSEQPDVEPDTLQKQA 734
+ H+ L YTHFTSPIRR+ D++VHRL+ +G + P + LQK
Sbjct: 549 -----SENNEGHFGLAAENYTHFTSPIRYP DLLVH RLI-REIGEGKTP---ANILQKWE 599

Query: 735 D 735
D
Sbjct: 600 D 600

>gi|21754656|dbj|BAC04542.1| unnamed protein product [Homo sapiens]
Length = 750

Score = 205 bits (521), Expect = 3e-51
Identities = 133/383 (34%), Positives = 197/383 (51%), Gaps = 32/383 (8%)

Query: 265 LFS PSDHRV PRIYVPLKDCP--QDFMTRPKDFANTLFICRIIDWKEDCNF ALGQLAKSLG 322
L +P D+R+P+I + + QDF + RI W+ + G + LG
Sbjct: 366 LVTPWDYRIPKIRISTQQAETLQDFRV-----VVRIDS WESTS VYPNGHFVRVLG 415

Query: 323 QAGEIEPETEGILTEYGVDFSDSSEVLECLPQSL---PWTIPPDEVGKRRDLRKD-CIF 378
+ G++E E IL E + FS + +P + PW + P+E KR+DLRK +F
Sbjct: 416 RIGDLEG EIATIL VENSISVIPFSEAQMCEMPVNTPESPW KVSPEEEQKRKDLRKSHLVF 475

Query: 379 TIDPSTARLDLDDALACRRLTDGTFEVGVIADVSYFVPEGSSLKDVAERATSVYLVQKV 438
+ IDP D+DD L+ R L +G E+GVHIADV++FV S +D A RAT+ YL +
Sbjct: 476 SIDPKGCEDVDDTLSVRTLNNGNLELG VHIADV THFVAPNSYIDIEARTRATTYYLADRR 535

Query: 439 VPMLP RLLCEELCSLNPMTDKLTFSVIWKLTPEG-KILEEWFGRTIIRSCTKLSYDHAQS 497
MLP +L +LCSL D+ S++W+L +I + W+GRTIIRS KL Y+ AQ
Sbjct: 536 YDMLPSVLSADLC SLLGGVDRYAVSIMWELDKASYEIKKVWYGR TIIRSAYKLFYEAQ E 595

Query: 498 MIENXXXXXXXXXXXXHS---VEEVHQAVLNLSIAKQLRRQRFVDGALRLDQLK 553
Sbjct: 596 LLDGNLSSVDDIPEFKDLGEKSRQAKLEELVWAIGKLTDIARHRAKRDGCGALELEGVE 655

Query: 554 LAFTLD----HETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRH 608
Sbjct: 656 VCVQLDDKKNIHDLIPKQPLEVHE----TVAECMILANHWWAKKIWESFPHQALLRQH 709

Query: 609 PPPQTKMLSDLVEFCDQMGLPMD 631
Sbjct: 710 PPPHQEFFSELRECAKAKGFFID 732

Score = 59.3 bits (142), Expect = 3e-07
Identities = 33/82 (40%), Positives = 51/82 (62%), Gaps = 8/82 (9%)

Query: 50 FETYMSKEDVSEGLKRGTLIQGVLRINPKKFH-EAFI----PSPDGD--RDIFIDGVVA 101
Sbjct: 225 YPEHLPLEVLEAGIKSGRYIQGILNVNKHRAQIEAFVRLQGASSKDSLVDILIHGMKA 284

Query: 102 RNRALNGDLVVVKLLPEDQWKA 123
Sbjct: 285 RNRSIHGDVVVVELLPKNEWKG 306

>gi|23020108|gb|ZP_00059814.1| hypothetical protein [Clostridium thermocellum ATCC 27405]
Length = 757

Score = 203 bits (516), Expect = 1e-50
Identities = 153/510 (30%), Positives = 245/510 (48%), Gaps = 50/510 (9%)

Query: 232 KVYYILEKK---HSRAATGILKLLADKNSDLF-----KKYALFSPSDHRVP-RIYVPLK 281
Sbjct: 108 RVIARINKKGIGDKRAEGEIIKIVKRANKTVVGTFESSKYFGFVVPDDPRISGDIIFI-- 164

Query: 282 DCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGV 341
Sbjct: 165 --PKDEINGAK--SGQKVVAEIVVWPEKRRNAEGRIIEIIIGDKDEPGSDILSIIKAYNLR 220

Query: 342 FSDFSSEVLECLPQLPWTIPPDEVGKRRDLRKDCIFTIDPSTARLDLACRRLTDGT 401
Sbjct: 221 -EDFPPEEVIR-EAKSISQTVTEDMIKGRRDLRDLTMVTIDGEDAKDLDDAVSIERLPNGN 278

Query: 402 FEVGVHIADVSYFPEGSSLKDVAERATSVYLVQKVVPMPLPRLLCHEELCSLNPMTDKLT 461
Sbjct: 279 YRLGVHIADVSYYVKEGSPLDKEALKRGTSVYLVDRVIPMFPKELSNGICSLNPKVDR 338

Query: 462 FSVIWKLTPEGKILEEWFGRTIIRSCTKLSYDHQSMEIENXXXXXXXXXXXXHSVE 521
Sbjct: 339 FTVMMEIDKSGRVVDHEIFESVINVNERMTYTDVYKILEENDEGLIERYKYLCDTFHTMK 398

Query: 522 EVHQAVLNLSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVE 581
Sbjct: 399 E-----LALILRKKRMDRGAIDFNFDEAKIVLD-EKGVPIEVKRYEMTIANNIIE 447

Query: 582 EFMLLANMAVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKS 641
Sbjct: 448 EFMLVCNETVAEHFFWT-NTPFVYRIHEDPDPDKIEAFSEFVHNLGYTLK----GINKI 501

Query: 642 LTKTFGD--DKYSLARKE-VLTNMYSRPMQMALY--FCSGMLQDQEQRHYALNVPLYTH 696
Sbjct: 502 HPKALQDVLEKARGTKEETIISTVMLRSLQKARYSHINSG-----HFGLAAKYYCH 552

Query: 697 FTSPIRRFADVIVHRLAALGYSEQPDVE 726

FTSPIRR+ D+I+HR++ L + P+ E
Sbjct: 553 FTSPIRRYPDLIIHRIMKEYLKGTVNPERE 582

>gi|16801605|ref|NP_471873.1| similar to exoribonuclease RNase-R [Listeria innocua]
gi|25298866|pir||AB1750 exoribonuclease RNase-R homolog lin2543 [imported]
- Listeria
innocua (strain Clip11262)
gi|16415065|emb|CAC97770.1| similar to exoribonuclease RNase-R [Listeria innocua]
Length = 793

Score = 201 bits (512), Expect = 3e-50
Identities = 138/430 (32%), Positives = 219/430 (50%), Gaps = 39/430 (9%)

Query: 313 ALGQLAKSLGQAGEIEPETEGILTEYGVDFSDSSEVLECLPQSLPWTIPPDEVGKRRDL 372
A G + +G + + I+ ++G+ + F EV+E + ++ P + ++G RRDL
Sbjct: 195 ARGVVKSIIGHRNDPGVDILSIIHKHGISA-FPEEVMEQVSKA-PDVVDDSDIGNRRDL 252

Query: 373 RKDCIFTIDPSTARLDL DALACRRLTDGT FEVGVHIA DVSYF VPEGSSLDKVA AERAT SV 432
R I T ID + A+DLDDA+ ++L +G +++GVH IADV+++V EGS LDK A +R TSV
Sbjct: 253 RDQMIITIDGADAKDLDDAVTVKQLPNGNWKLGVHIA DVTHYVTEGSP LDKEA QDRG TS V 312

Query: 433 YLVQKVVPMLP RLLCEELCSLNPM TDKLTFSVIWKL TPEGKILEEWFGRTI IRSCT KLSY 492
YLV +V+PMLP L +CSLNP D+ T S ++ EG ++ +II++ +++Y
Sbjct: 313 YLVDRVIPMLPHKLSNGICSLNPQVDRFTMSCEMEIDQEGHV VNHEIFESI IKTTERMTY 372

Query: 493 DHAQSMIENXXXXXXXXXXXXXXHSVEEVHQAVLN LHSIAKQLRRQRFVDGALR LDQL 552
++ + + + +A+ LRR+R GA+ D
Sbjct: 373 TDVNDILVEKDEALREKYAPIVPMLEAMQH-----LAEILRRKREKRGAI DF D-F 421

Query: 553 KLAFTLDHETGLPQGCHIYEYRDSNKLVEEFML LANMAVAHKIFRTFPEQALLRRH PPPQ 612
K A + E G P+ + E L+EEFML AN VA F + R H P+
Sbjct: 422 KEARVVVDEEGHPEEVVMRERSAGEHLIEEFMLAANETVAEH-FHWMDVPFIYRIHEDPK 480

Query: 613 TKMLSDLVEFCDQMGLPMDVSSAGALNKS LT KTFGDDKYS LARKEV LTNMYSRPMQ M ALY 672
L+ EF GL + K +D + A ++VL + +P +M +
Sbjct: 481 EDKLARFFEFITNFGL-----IVKGTANDIHPAALQQVLEEVKGKPEEMVV- 526

Query: 673 FCSGMLQDQE QFR-----HYALNVPLYTHFTSPIR RFAD VIVHRL LAA ALGYSEQPDV 725
+ ML+ +Q + H+ L+ YTHFTSPIR+ D+IVHRL+ Y DV
Sbjct: 527 -STVMLRSMQQAKYDTVSAGH FGLSTD FYTHFTSPIR RY PDLIVHRLIRE---YLINGDV 582

Query: 726 EPDTLQKQAD 735
P+TL+K+A+
Sbjct: 583 RPETLEKRAE 592

>gi|16804487|ref|NP_465972.1| similar to exoribonuclease RNase-R [Listeria monocytogenes EGD-e]
gi|25298867|pir||AI1380 exoribonuclease RNase-R homolog lmo2449 [imported]
- Listeria
monocytogenes (strain EGD-e)
gi|16411937|emb|CAD00527.1| similar to exoribonuclease RNase-R [Listeria monocytogenes]
Length = 793

Score = 200 bits (509), Expect = 7e-50
Identities = 138/430 (32%), Positives = 218/430 (50%), Gaps = 39/430 (9%)

Query: 313 ALGQLAKSLGQAGEIEPETEGILTEYGVDFSDSSEVLECLPQSLPWTIPPDEVGKRRDL 372
A G + +G + + I+ ++G+ F EV+E + ++ P + ++G RRDL
Sbjct: 195 ARGVVKSIIGHRNDPGVDILSIIHKHGISA-FPEEVMEQVSKA-PDVVDDSDIGNRRDL 252

Query: 373 RKDCIFTIDPSTARLDL DALACRRLTDGT FEVGVHIA DVSYF VPEGSSLDKVA AERAT SV 432
R I T ID + A+DLDDA+ ++L +G +++GVH IADV+++V EGS LDK A ER TSV

Sbjct: 253 RDQMIITIDGADAKDLDDAVTVKQLPNGNWKLGVHIADVTHYVTEGSPLDIEAQERGTSV 312

Query: 433 YLVQKVVPMLPRLLCIELCSLNPMTDKLTFSVIWKLTPPEGKILEEWFGRTIIRSCTKLSY 492
YLV +V+PMLP L +CSLNP D+ T S ++ EG ++ +II++ +++Y

Sbjct: 313 YLVDRVIPMLPHKLSNGICSLNPQVDRFTMSCEMEIDQEGHVVNHEIFESIICKTERMTY 372

Query: 493 DHAQSMIENXXXXXXXXXXXXXXHSVEEVHQAVNLHSIAKQLRRQRFVDGALRDLQ 552
++ +++ +A+ LRR+R GA+ D

Sbjct: 373 TDVNNDILVEKDEALREKYAPIVPMLEAMQ-----NLAEILRRKREKRGAIKFD-F 421

Query: 553 KLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPQ 612
K A + E G P+ + E L+EEFML AN VA F + R H P+

Sbjct: 422 KEARVVVDEDGHPEAVVMRERSAGEHLIEEFMLAANETVAEH-FHWMDVPFIYRIHEDPK 480

Query: 613 TKMLSDLVEFCDQMGLPMDVSSAGALNKS LT KTFGDDKYSLARKEVL TNMYSRPMQMALY 672
L+ EF GL + K +D + A ++VL + +P +M +

Sbjct: 481 EDKLARFFEFITNFGL-----IVKGTANDIHPAALQQVLEEVKGKPEEMVV- 526

Query: 673 FCSGMLQDQEQR-----HYALNVPLYTHFTSPIRRFADVIVHRL LAAALGYSEQPDV 725
+ ML+ +Q + H+ L+ YTHFTSPIRR+ D+IVHRL+ Y DV

Sbjct: 527 -STVMLRSMQQAKYDTVSAGHFGLSTDYTHFTSPIRRYPDLIVHRLIRE--YLINGDV 582

Query: 726 EPDTLQKQAD 735
P+TL+K+A+

Sbjct: 583 RPETLEKRAE 592

>gi|21397569|ref|NP_653554.1| RNB, RNB-like protein [Bacillus anthracis A2012]
Length = 808

Score = 197 bits (501), Expect = 7e-49
Identities = 133/414 (32%), Positives = 214/414 (51%), Gaps = 22/414 (5%)

Query: 300 ICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDSSEVLECLPQSLPW 359
+ +I + E+ A G++ + LG + + ++ ++ + + F EV+E S+P

Sbjct: 185 VVKITSYPENRLSAEGERVIQILGHKNDPGVDILSVIHKHHLPLA-FPEEVME-HANSVPE 242

Query: 360 TIPPDEVGKRRDLRKDCIFTIDPSTARLDDALACRRLTDGTFEVGVHIADVSYFVPEG 419
TI +++ RRDLR I TID + A+DLDDA+ +L +G +--+GVHIADVS++V EGS

Sbjct: 243 TISEEDLKDRDLDQMVITIDGADAKDLDDAVTVKLENGNYKLGVHIADVSHYVQEGS 302

Query: 420 SLDKVAERATSVYLVQKVVPMLPRLLCIELCSLNPMTDKLTFSVIWKLTPPEGKILEEWF 479
+D AAERATSVYLV +V+PM+P L +CSLNP D+LT S ++ G'++
Sbjct: 303 PIDVEAAERATSVYLVDRVIPMIPHRLSNGICSLNPKVDRTLSCEMEINNLGDVVKHEI 362

Query: 480 GRTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXHSVEEVHQAVNLHSIAKQLRR 539
+++I++ +++Y +S++E+ E + + +A+ LR

Sbjct: 363 FQSVIKTTERMTYADVRSILEDDEELMKRY-----EPLVPMFKEMGQLAQILRE 412

Query: 540 QRFVGDALRDLQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTF 599
+R GA+ D K A L E G P + + S KL+EEFML+AN VA F

Sbjct: 413 KRMRRGAIDFD-FKEAKVLVDEEGKPTDVVMRDRSVSEKLIIEFMLVANETVAEH-FHWM 470

Query: 600 PEQALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKS LT KTFGDDKYSLARKEVL 659
+ R H P+ L EF G + + ++L + + + V+
Sbjct: 471 NVPFMYRVHEDPKEDKLERFFEFVTNFGYAVKGRANEVHPRALQQIL-EMVQGQPEEVVI 529

Query: 660 TNMYSRPMQMALYFCGMLQDQEQRHYALNVPLYTHFTSPIRRFADVIVHRL 713
+ + R M+ A Y D + H+ L+ YTHFTSPIRR+ D IVHRL+

Sbjct: 530 STVMLRSMKQARY-----DADSLGHFGLSTEFYTHFTSPIRRYPDTIVHRLI 576

>gi|16080414|ref|NP_391241.1| similar to hypothetical proteins [Bacillus subtilis]
gi|7674332|sp|O32231|RNR_BACSU Ribonuclease R (RNase R) (VacB protein homolog)

gi|7443068|pir||G70027 conserved hypothetical protein yvaJ - Bacillus subtilis
gi|2635874|emb|CAB15366.1| similar to hypothetical proteins [Bacillus subtilis]
Length = 779

Score = 195 bits (495), Expect = 3e-48
Identities = 131/418 (31%), Positives = 213/418 (50%), Gaps = 22/418 (5%)

Query: 300 ICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDSSEVLECLPQLPW 359
+ ++ + E A G++ LG + + ++ ++G+ +F ++ +E S P
Sbjct: 181 VVKLTSYPEGRMNAEGEREVETILGHKNDPGIDILSVIHKHGLP-GEFPADAME-QASSTPD 238

Query: 360 TIPPDEVGKRRDLRKDCIFTIDPSTARLDLACRRLTDGTFEVGVHIADVSYFVPEGS 419
TI ++ RRDLR I TID + A+DLDDA+ +L DG++++GVHIADVS++V E S
Sbjct: 239 TIDEKDLKDRRDLRDQVIVTIDGADAKDLDDAVTVTKLDDGSYKLGVHIADVSHVTENS 298

Query: 420 SLDKVAERATSVYLVQKVVPMPLPRLLCEELCSLNPMTDKLTFSVIWKLTPKGKILEEWF 479
+DK A ER TSVYLV +V+PM+P L +CSLNP D+LT S + +G++ E
Sbjct: 299 PIDKEALERGTSVYLVDRVIPMIPHRLSNGICSLNPVDRTLSCEMTINSQGQVTEHEI 358

Query: 480 GRTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXHSVEEVHQAVNLHSIAKQLRR 539
+++I++ +++Y ++ + E + ++ +A+ LR
Sbjct: 359 FQSVIKTTERMTYSDVNKILVD-----DDEELKQKYEPLVPMFKDMERIAQILRD 408

Query: 540 QRFVGDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVHKIFRTF 599
+R GA+ D K A L + G + I E + KL+EEFML+AN VA F
Sbjct: 409 KRMDRGAVDFD-FKEAKVLVDDEGAVKDVVIRERSVAEKLIEEFMLVANETVAEH-FHWM 466

Query: 600 PEQALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKS LT KTFGDDKYSLARKEVL 659
+ R H P + L +EF G + +AG ++ + + D + V+
Sbjct: 467 NVPFIYRIHEEPNAEKLQKFLEFVTTFGYVVK-GTAGNIHPRALQSILDAVRDRPEETVI 525

Query: 660 TNMYSRPMQMALYFCGMLQDQEQRHYALNVPLYTHFTSPIRFADIVVHRLAAL 717
+ + R M+ A Y D + H+ L+ YTHFTSPIRR+ D+IVHRL+ L
Sbjct: 526 STVMLRSMKQAKY-----DPQSLGHFGLSTEFYTHFTSPIRYPDLIVHRLIRTYL 576

>gi|15894003|ref|NP_347352.1| FUSION ribonuclease and ribosomal protein S1 domain [Clostridium acetobutylicum]
gi|25298861|pir||A96988 FUSION ribonuclease and ribosomal protein S1 domain [imported] - Clostridium acetobutylicum
gi|15023595|gb|AAK78692.1|AE007586_9 FUSION ribonuclease and ribosomal protein S1 domain [Clostridium acetobutylicum]
Length = 730

Score = 190 bits (483), Expect = 7e-47
Identities = 128/420 (30%), Positives = 213/420 (50%), Gaps = 35/420 (8%)

Query: 300 ICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDSSEVLECLPQLPW 359
+ I W + G++ + +G GE + I+ ++ + E +E + +P
Sbjct: 177 VAEITVWPKKRRNPEGKIVEIIGSKGEKGVDILTIKKH--KLPEKFPEKVERFAEGIPN 234

Query: 360 TIPPDEVGKRRDLRKDCIFTIDPSTARLDLACRRLTDGTFEVGVHIADVSYFVPEGS 419
IP E +RRD+R + TID A+DLDDA++ +L+G F++GVHIADVS +V E +
Sbjct: 235 EIPESEYKRRRDIRDVKMVTIDGEDAKDLDDAVSIEKLSNGNFKLGVHIADVSNVREDN 294

Query: 420 SLDKVAERATSVYLVQKVVPMPLPRLLCEELCSLNPMTDKLTFSVIWKLTPKGKILEEWF 479
LDK A +RATSVYL+ +V+PMPL+ L +CSLNP D+L S ++ P GK+++
Sbjct: 295 PLDKEALKRATSVYLIIDRVIPMLPKLNSNGICSLNPQDRLAMSCFMEIDPTGKVIQHEI 354

Query: 480 GRTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXHSVEEVHQAVNLHSIAKQLRR 539
+II++ +++Y ++ + + E ++ N+ +A L +

Sbjct: 355 FESIIKTNERMTYTDVTKILRD-----HDEETIKAFELYDDFKNMEELASILNK 404
Query: 540 QRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVA-HKIFRT 598
+R + GA+ D + TL+ E G P YE +N+++EEFML+ N +A H +
Sbjct: 405 KRLLRGAIDFDFEESKITLN-ELGKPVEVKPYERAVANRIIEEFMLVCNETIAEHFYWAN 463
Query: 599 FPEQALLRRHPPPQTKMLSDLVEFCDQMGLPMVDVSS---AGALNKS LT KTFGDDKYSLAR 655
P + R H P ++ L EF +G + S L + K G +
Sbjct: 464 IP--FVYRVHEEPDSEKLERFNEFIHNLGYAVRWGSEVHPQLQDVIEKIKGKKE---- 516
Query: 656 KEVLTNMYSRPMQM ALYF--CSGMLQDQEQRHYALNVPLYTHFTSPIRRFAD VIVHRL 713
+ V++ + R ++ A Y CSG H+ L Y HFTSPIRR+ D+I+HR++
Sbjct: 517 ETVVSTLLLRSLKQARYSPEC SG-----HFGLAARYYCHFTSPIRYPDLIIHRIM 567

>gi|27467483|ref|NP_764120.1| ribonuclease R [Staphylococcus epidermidis ATCC 12228]
gi|27315026|gb|AAO04162.1|AE016745_261 ribonuclease R [Staphylococcus epidermidis ATCC 12228]
Length = 792

Score = 190 bits (483), Expect = 8e-47
Identities = 132/430 (30%), Positives = 215/430 (50%), Gaps = 26/430 (6%)

Query: 315 GQLAKSLGQAGEIEPETEGILTEYGVDFSD FS SEVLECL PQSLPWTIPPDEVGKRRDLRK 374
G ++ LG + + I+ ++G++ +F +VL+ + +P I P E+ RRDLR
Sbjct: 199 GHVSAILGHKNDPGVDILSIIYQHGIEI-EFPDDVLQ-EAEEVPD VIEPSEIEGRRL RD 256
Query: 375 DCIFTIDPSTAR DALACRRLTDGT FEVG VHIADV SYFVPEGSSL DKVAAERAT SVYL 434
+ TID + A+DLDDA+A ++L +G E+ V IADSY+V EGS+LDK A +RAT SVYL
Sbjct: 257 ELTITIDGADAKDLDDAI AVKKLKGNGNTELTVSIADVSYYVKEGSALDKEAYDRAT SVYL 316
Query: 435 VQKVVPMLP RLLCEELCS LNPMTDKLTFSVIWKLTPEGKILEEWFGRTIIRSCTKLSYDH 494
V +V+PM+P L +CSLNP D+LT S ++ G++++ ++I S +++YD
Sbjct: 317 VDRVIPMI PHRLSNGICSLNPEEDRLTLSCRMEINERGEVV KHEIFDSVIHSNYRMTYDA 376
Query: 495 AQSMIENXXXXXXXXXXXXXHSVEEVHQAVLN LHSIAKQLRRQRFVDGALRLDQLKL 554
+I + ++ ++ +L R R G + D +
Sbjct: 377 VNKIITDQDSEIRS QYKDLTPMLD LAQD-----LSNR LIRMRKRRGEIDFD-INE 425
Query: 555 AFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQTK 614
A L ++ G+P + E + +L+E FML AN VA F + R H P++
Sbjct: 426 AKVLVNDEGIPTEVLMRERGEGERLIESFMLAANETVAEH-FNKLEV PFIYRVHEQPKSD 484
Query: 615 MLS DLVEFCDQMGLPM DVSSAGALNKS LT KTFGDDKYSLARKEVLTN MYSRPMQM ALYFC 674
L +F G+ M + ++ + + ++ + V++ M R MQ A Y
Sbjct: 485 RLRQFFDFITNFGI-MIKGTGEDIHPTTLQNIQEEVEGRPEQM VISTMMMLRSMQQAHY-- 541
Query: 675 SGMLQDQEQRHYALNVPLYTHFTSPIRRFAD VIVHRL LAAALGYSE QPDVE----PDTL 730
D H+ L+ YTHFTSPIRR+ D+ VHRL+ L + E +TL
Sbjct: 542 ----DDVNLGHFGLSAEYYTHFTSPIRYPDLTVHRLIRKYLIENSMDKKEIRHWEETL 596
Query: 731 QKQADHCNDR 740
+ A+H + R
Sbjct: 597 PELAEHTSQR 606

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF
Posted date: Jan 29, 2003 9:26 AM
Number of letters in database: 423,161,544
Number of sequences in database: 1,321,324

Lambda K H
0.319 0.136 0.399

Gapped

Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 681,347,984

Number of Sequences: 1321324

Number of extensions: 28649337

Number of successful extensions: 62317

Number of sequences better than 10.0: 242

Number of HSP's better than 10.0 without gapping: 232

Number of HSP's successfully gapped in prelim test: 10

Number of HSP's that attempted gapping in prelim test: 61354

Number of HSP's gapped (non-prelim): 402

length of query: 870

length of database: 423,161,544

effective HSP length: 132

effective length of query: 738

effective length of database: 248,746,776

effective search space: 183575120688

effective search space used: 183575120688

T: 11

A: 40

X1: 16 (7.4 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 41 (21.7 bits)

S2: 77 (34.3 bits)